

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:59 ; Search time 9.5 Seconds
(without alignments)
7.985 Million cell updates/sec

Title: 09937009-B

Sequence: 1 fpqfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
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2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB pep: *
3: /EMC_Celerra_SIDS3/prodata/1/pubppa/US07_NEW_PUB pep: *
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7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB pep: *
8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	480	US-10-511-814-6	Sequence 6, Appli
2	28	80.0	15	US-11-118-524-4	Sequence 4, Appli
3	28	80.0	109	US-11-293-697-2693	Sequence 2693, Ap
4	28	80.0	147	US-10-953-349-5010	Sequence 5010, Ap
5	28	80.0	170	US-10-953-349-26194	Sequence 26194, A
6	28	80.0	181	US-10-953-349-5009	Sequence 5009, Ap
7	28	80.0	185	US-10-953-349-26193	Sequence 26193, A
8	28	80.0	203	US-10-953-349-5008	Sequence 5008, Ap
9	28	80.0	247	US-10-953-349-27950	Sequence 27950, A
10	28	80.0	334	US-10-953-349-30809	Sequence 30809, A
11	28	80.0	336	US-10-953-349-35132	Sequence 35132, A
12	28	80.0	370	US-10-953-349-30808	Sequence 30808, A
13	28	80.0	376	US-10-953-349-35131	Sequence 35131, A
14	28	80.0	585	US-10-953-349-7243	Sequence 7243, Ap
15	28	80.0	590	US-10-953-349-7242	Sequence 7242, Ap
16	28	80.0	593	US-10-953-349-7241	Sequence 7241, Ap
17	28	80.0	705	US-11-242-317-43	Sequence 43, Appli
18	28	80.0	4373	US-11-118-524-2	Sequence 2, Appli
19	27	77.1	264	US-10-953-349-22672	Sequence 22672, A
20	27	77.1	328	US-10-953-349-22671	Sequence 22671, A
21	27	77.1	302	US-10-953-349-18719	Sequence 18719, A
22	27	77.1	322	US-10-953-349-18839	Sequence 18839, A
23	27	77.1	337	US-10-953-349-22670	Sequence 22670, A
24	27	77.1	356	US-10-953-349-18838	Sequence 18838, A
25	27	77.1	369	US-10-953-349-18837	Sequence 18837, A

ALIGNMENTS

26	27	77.1	390	6	US-10-953-349-18718	Sequence 18718, A
27	27	77.1	395	6	US-10-953-349-18717	Sequence 18717, A
28	27	77.1	916	6	US-10-186-749-78	Sequence 78, Appli
29	26	74.3	36	6	US-10-953-349-15240	Sequence 15240, A
30	26	74.3	145	6	US-10-953-349-29947	Sequence 29947, A
31	26	74.3	181	6	US-10-953-349-29946	Sequence 29946, A
32	26	74.3	192	6	US-10-953-349-19801	Sequence 19801, A
33	26	74.3	194	6	US-10-953-349-7305	Sequence 7305, Ap
34	26	74.3	201	7	US-11-293-697-3199	Sequence 3199, Ap
35	26	74.3	246	6	US-10-953-349-28145	Sequence 28145, A
36	26	74.3	281	6	US-10-953-349-33611	Sequence 33611, A
37	26	74.3	283	6	US-10-953-349-33610	Sequence 33610, A
38	26	74.3	286	6	US-10-953-349-31389	Sequence 31389, A
39	26	74.3	288	6	US-10-953-349-7304	Sequence 7304, Ap
40	26	74.3	299	6	US-10-953-349-28144	Sequence 28144, A
41	26	74.3	314	6	US-10-953-349-5664	Sequence 5664, Ap
42	26	74.3	315	6	US-10-953-349-5663	Sequence 5663, Ap
43	26	74.3	325	6	US-10-953-349-23130	Sequence 23130, A
44	26	74.3	339	6	US-10-953-349-33609	Sequence 33609, A
45	26	74.3	340	6	US-10-953-349-31388	Sequence 31388, A

RESULT 1
US-10-511-814-6
Sequence 6, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
APPLICANT: McCance, Dennis
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12567
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 480
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-6
Query Match 100.0%; Score 35; DB 6; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FPQFSY 6
Db 469 FPQFSY 474
RESULT 2
US-11-118-524-4
Sequence 4, Application US/11118524
Publication No. US2006008847A1
GENERAL INFORMATION:
APPLICANT: GU, WEI
TITLE OF INVENTION: ARF-BP1 AS MEDIATOR OF P53-DEPENDENT AND INDEPENDENT TUMOR
FILE REFERENCE: 19240-497US2
CURRENT APPLICATION NUMBER: US/11/118,524
CURRENT FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: 60/610,506
PRIOR FILING DATE: 2004-09-15

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/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 4
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-118-524-4
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Query Match      80.0%; Score 28; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 PPOFS 5
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Db       8 PPOFS 12
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RESULT 3
US-11-293-697-2693
/ Sequence 2693, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
```

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/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ CURRENT FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2693
/ LENGTH: 109
/ TYPE: PRT
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/ ORGANISM: Homo sapiens
US-11-293-697-2693
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Query Match      80.0%; Score 28; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 PPOFS 5
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Db       61 PPOFS 65
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RESULT 4
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US-10-953-349-5010
/ Sequence 5010, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5010
/ LENGTH: 147
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-953-349-5010
```

```
Query Match      80.0%; Score 28; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db       9 PPOFS 13
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RESULT 5
US-10-953-349-26194
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/ Sequence 26194, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26194
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-953-349-26194
```

```
Query Match      80.0%; Score 28; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db      142 PPOFS 146
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RESULT 6
US-10-953-349-5009
/ Sequence 5009, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
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/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5009
/ LENGTH: 181
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-953-349-5009
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Query Match      80.0%; Score 28; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 PPOFS 5
        |||||
Db       43 PPOFS 47
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RESULT 7
US-10-953-349-26193
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```
/ Sequence 26193, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nikolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26193
/ LENGTH: 185
/ TYPE: PRT
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ORGANISM: Trilicium aestivum
US-10-953-349-26193

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 185;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 157 PPOFS 161

RESULT 8

US-10-953-349-5008
; Sequence 5008, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5008
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5008

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 203;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 65 PPOFS 69

RESULT 9

US-10-953-349-27950
; Sequence 27950, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27950
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-27950

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 247;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPOFS 6
Db 227 PPOFS 232

RESULT 10

US-10-953-349-30809
; Sequence 30809, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30809
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-30809

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 334;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 85 PPOFS 89

RESULT 11

US-10-953-349-35132
; Sequence 35132, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35132
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35132

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 336;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
Db 87 PPOFS 91

RESULT 12

US-10-953-349-30808
; Sequence 30808, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30808
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-30808

Query Match
Best Local Similarity 80.0%; Score 28; DB 6; Length 370;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
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Db 121 PPOFS 125

RESULT 13

US-10-953-349-35131
; Sequence 35131, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35131
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35131

Query Match 80.0%; Score 28; DB 6; Length 376;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFS 5
|||
Db 127 PPOFS 131

RESULT 14

US-10-953-349-7243
; Sequence 7243, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7243
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7243

Query Match 80.0%; Score 28; DB 6; Length 585;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
||:|
Db 29 PPEFSF 34

RESULT 15

US-10-953-349-7242
; Sequence 7242, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7242
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7242

Query Match 80.0%; Score 28; DB 6; Length 590;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
||:|
Db 34 PPEFSF 39

Search completed: June 14, 2006, 02:38:22
Job time : 10.5 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:09:23 ; Search time 24 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fpqfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	479	A59380	protein kinase (EC
2	35	100.0	480	A39360	protein kinase (EC
3	35	100.0	480	JC2437	protein kinase (EC
4	35	100.0	480	S33364	protein kinase (EC
5	35	100.0	480	S62117	protein kinase (EC
6	35	100.0	481	A46288	protein kinase (EC
7	35	100.0	481	JC2438	protein kinase (EC
8	35	100.0	611	A55888	protein kinase (EC
9	35	100.0	763	A40831	gag-akt polyprote
10	32	91.4	270	T40280	26S proteasome reg
11	32	91.4	655	T39064	RNA binding protei
12	31	88.6	241	B71128	probable iron (III
13	31	88.6	303	H35068	apolipoprotein H-r
14	31	88.6	348	1	matrix protein - S
15	31	88.6	348	1	matrix protein - S
16	31	88.6	348	1	matrix protein - S
17	31	88.6	452	2	complement factor
18	31	88.6	453	2	complement factor
19	31	88.6	669	2	probable exported
20	31	88.6	682	2	hypothetical prote
21	31	88.6	808	2	complement factor
22	31	88.6	1234	1	complement factor
23	30	85.7	241	2	hypothetical prote
24	30	85.7	302	2	GAD65 family prote
25	30	85.7	302	2	hypothetical prote
26	30	85.7	413	2	hypothetical prote
27	30	85.7	474	2	hypothetical prote
28	30	85.7	583	2	phosphoglucosidase
29	30	85.7	627	2	hypothetical prote

ALIGNMENTS

30	30	85.7	785	2	T11719	probable vacuolar
31	30	85.7	858	2	S50730	hypothetical prote
32	30	85.7	1718	2	T31638	hypothetical prote
33	29	82.9	32	2	S20275	32k protein - Rhod
34	29	82.9	74	2	S16868	gene I3 protein -
35	29	82.9	81	2	S01059	hypothetical prote
36	29	82.9	107	2	G69998	chirodoxin H1 hom
37	29	82.9	151	2	B84751	hypothetical prote
38	29	82.9	159	2	AC0338	probable colicin V
39	29	82.9	332	2	C84061	ferichrome ABC tr
40	29	82.9	374	2	E83843	hypothetical prote
41	29	82.9	445	2	AE1590	hypothetical prote
42	29	82.9	445	2	AE1590	weakly methyltrans
43	29	82.9	446	2	H95072	hypothetical prote
44	29	82.9	446	2	G97940	hypothetical prote
45	29	82.9	458	2	F97146	probable iron-bullf

RESULT 1

A59380 protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C>Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: A59380; A59379
J:Brodebeck, D.; Cron, P.; Hemmings, B.A.
R: Biol. Chem. 274, 9133-9136, 1999
A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti
A:Reference number: A59380; PMID:99194749; PMID:10092583
A:Accession: A59380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <BRO>
A:Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335B8; GB:AM29089; NID:94757579; PII
R:Masure, S.; Haefner, B.; Weselink, J.J.; Hofnagel, E.; Mortier, E.; Verhasselt, P.; J
Eur. J. Biochem. 265, 353-360, 1999
A:Title: Molecular cloning, expression and characterization of the human serine/threonine
A:Reference number: A59379; PMID:99421751; PMID:10491192
A:Accession: A59379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <MAS>
A:Cross-references: UNIPARC:UPI00000335B8; GB:CAB53537; NID:95804886; PIDN:CAB53537.1
C:Genetics:
A:Gene: GDB:AKT3; PKBG; PRKBG; RAC-gamma
A:Cross-references: GDB:9954867
A:Map position: 1q44-1q44
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein }
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:7-108/Domain: pleckstrin repeat homology <PLK>
F:149-408/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif
F:177/Active site: lys #status predicted
F:305/Binding site: phosphate (Thr) (covalent) #status predicted
F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPQFSY 6
DB 468 FPQFSY 473

RESULT 2
A39360

protein kinase (EC 2.7.1.37) akt1 [validated] - human
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Homo sapiens (man)
 C:Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
 C:Accession: A39360; S36389; S18000; S20836
 R:Jones, P.F.; Jakubowicz, T.; Pilossi, P.D.; Maurer, F.; Hemmings, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
 A:Title: Molecular cloning and identification of a serine/threonine protein kinase of th
 A:Reference number: A39360; PMID:91239529; PMID:1851997
 A:Accession: A39360
 A:Molecule type: mRNA
 A:Residues: 1-480 <ON>
 A:Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E755; GB:M63167; NID:g190827; PIDN:
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A:Reference number: S24423; PMID:92249329; PMID:1533586
 A:Contents: erratum
 A:Accession: S36389
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '
 A:Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA3372.1; PID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinas
 A:Reference number: S17999; PMID:92037600; PMID:1718748
 A:Accession: S18000
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 63-70, 'TPSSSAACSGPLSSNAPMRLNSGGVNDHHPDGRPPQ', 'EAGGGGDLGVLGTORQLRGRDDGV
 A:Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037
 A:Note: this sequence has been revised in reference S24423
 R:Allesi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
 EMBO J. 15, 6541-6551, 1996
 A:Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
 A:Reference number: A64192; PMID:97133284; PMID:8978681
 A:Contents: annotation; phosphorylation sites
 R:Tokar, A.; Newton, A.C.
 J. Biol. Chem. 275, 8271-8274, 2000
 A:Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD
 A:Reference number: A64193; PMID:20187529; PMID:10722653
 A:Contents: annotation; autophosphorylation site
 C:Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy-1,3
 nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
 C:Genetics:
 A:Gene: GDB:AKT1; RAC; PKB
 A:Cross-references: GDB:118989; OMIM:164730
 A:Map position: 14q32.32-14q32.32
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Pathway: signal transduction pathways regulating various processes including insulin a
 e production
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase ATP-binding motif
 F:156-164/Region: protein kinase ATP-binding motif
 F:179/Active site: Lys #status predicted
 F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
 F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experime

Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPOFSY 6
 Db 469 PPOFSY 474
 RESULT 3
 JC2437
 protein kinase (EC 2.7.1.37) akt1 [validated] - rat
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
 C:Accession: JC2437
 R:Konishi, H.; Shimomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
 Biochem. Biophys. Res. Commun. 205, 817-825, 1994
 A:Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associatio
 A:Reference number: JC2437; PMID:95091823; PMID:7999118
 A:Accession: JC2437
 A:Molecule type: mRNA
 A:Residues: 1-480 <KON>
 A:Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DDBJ:D30040; NID:g485402; PID
 A:Experimental source: testis
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Pathway: signal transduction pathways regulating various processes
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase ATP-binding motif
 F:156-164/Region: protein kinase ATP-binding motif
 F:179/Active site: Lys #status predicted
 F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
 F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predictec
 Query Match 100.0%; Score 35; DB 1; Length 480;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPOFSY 6
 Db 469 PPOFSY 474
 RESULT 4
 S33364
 protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protei
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: S33364
 R:Bellacosa, A.; Franke, T.F.; Gonzalez-Porta, M.E.; Datta, K.; Taguchi, T.; Gardner, J.
 Oncogene 8, 745-754, 1993
 A:Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt ar
 A:Reference number: S33364; PMID:93173519; PMID:8437858
 A:Accession: S33364
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-480 <BEL>
 A:Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
 C:Genetics:
 A:Gene: MGI:AKT
 A:Cross-references: MGI:87986
 A:Map position: 12
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Pathway: signal transduction pathways regulating various processes
 C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene;
 F:4-106/Domain: pleckstrin repeat homology <PLK>
 F:148-408/Domain: protein kinase ATP-binding motif
 F:156-164/Region: protein kinase ATP-binding motif

F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 469 PPOFSY 474

RESULT 5

S62117
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N/Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C/Accession: S62117; S24423; S17999; S15714; S36388
R/Coffier, P.J.; Woodgett, J.R.
Submitted to the EMBL Data Library, December 1991
A/Reference number: S62117
A/Accession: S62117
A/Molecule type: mRNA
A/Residues: 1-480 <COF>

A/Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:9630; PIDN:C
A/Note: This is a revision to the sequence from reference S17999
R/Coffier, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A/Reference number: S24423; MUID:92249329; PMID:1533566
A/Contents: erratum
A/Accession: S24423
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 70-78, 'N', 80-145 <COM>

A/Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
A/Note: This is a revision to the sequence from reference S17999
R/Coffier, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A/Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A/Reference number: S17999; MUID:92037600; PMID:1718748
A/Accession: S17999
A/Molecule type: mRNA
A/Residues: 1-70, 'TPSSSAACGPRSSASRTRRRSGCVDRHHPDGGRRADGAGGDDGLFVGLTRRELGRGNDGVAGQK
A/Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036
A/Note: This sequence has been revised in references S62117 and S24423
C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein kinase
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 469 PPOFSY 474

RESULT 6

A46288
protein kinase (EC 2.7.1.37) akt2 - human
N/Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
C/Species: Homo sapiens (man)

C/Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004

C/Accession: A46288
R/Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; Thibodeau, N.A.; Acosta, S.; U.S.A. 89, 9267-9271, 1992
A/Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/threonine kinases
A/Reference number: A46288; MUID:93028445; PMID:1409633
A/Accession: A46288
A/Molecule type: mRNA
A/Residues: 1-481 <CHE>

A/Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M65936; NID:9178325; PIDN:J
A/Note: sequence extracted from NCBI backbone (NCBI:P.115859)
C/Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C/Genetics:
A/Gene: GDB:AKT2
A/Cross-references: GDB:135660; OMIM:164731
A/Map position: 19q13.2-19q13.2

C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein kinase
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 481;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 470 PPOFSY 475

RESULT 7

JC2438
protein kinase (EC 2.7.1.37) akt2 [validated] - rat
N/Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C/Accession: JC2438
R/Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A/Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A/Reference number: JC2437; MUID:95091823; PMID:7999118
A/Accession: JC2438
A/Molecule type: mRNA
A/Residues: 1-481 <KON>

A/Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D30041; NID:9485404; PIDN:J
A/Experimental source: testis
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes including myoblast
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein kinase
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 481;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
DB 470 PPOFSY 475

RESULT 8

A55888
protein kinase (EC 2.7.1.37) akt (similarity) - fruit fly (Drosophila melanogaster)

N/Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase RA
 C/Species: Drosophila melanogaster
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C/Accession: A55888
 R/Andjelkovic, M.; Jones, P.F.; Grosenklau, U.; Cron, P.; Schier, A.F.; Dick, M.; Bilh
 J. Biol. Chem. 270, 4066-4075, 1995
 A/Title: Developmental regulation of expression and activity of multiple forms of the D
 A/Reference number: A55888; MUID:95181376; PMID:7876156
 A/Accession: A55888
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-611 <MND>
 A/Cross-references: UNIPROT:Q24469; UNIPARC:UPI0000866BE; GB:X83510
 C/Genetics:
 A/Gene: FLYBase:RacPK
 A/Cross-references: FLYBase:FBgn013324
 A/Start codon: ACG
 A/Introns: 261/3; 327/3; 457/3; 535/3; 584/3
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A/Pathway: signal transduction pathways regulating various processes
 C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
 C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threoni
 F/105-209/Domain: pleckstrin repeat homology <PLK>
 F/264-523/Domain: protein kinase homology <KIN>
 F/272-280/Region: protein kinase ATP-binding motif
 F/295/Active site: Lys #status predicted
 F/423/Binding site: phosphate (Tn) (covalent) #status predicted
 F/586/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match

Best Local Similarity 100.0%; Score 35; DB 1; Length 611;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 Db 582 PPOFSY 587

RESULT 9

A40831
 gag-akt polypeptide - AKT8 murine leukemia virus
 N/Contains: amino end of core protein p10; core protein p15; inner coat protein p12; kin
 C/Species: AKT8 murine leukemia virus
 C/Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
 C/Accession: A40831
 R/Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.
 Science 254, 274-277, 1991
 A/Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH
 A/Reference number: A40831; MUID:92022574; PMID:1833819
 A/Accession: A40831
 A/Molecule type: DNA
 A/Residues: 1-262 <BEL>
 A/Cross-references: UNIPARC:UPI00001725AF; GB:M80675
 A/Accession: B40831
 A/Molecule type: DNA
 A/Residues: 262-763 <BE2>
 A/Cross-references: UNIPARC:UPI00001725B0; GB:M80675
 C/Genetics:
 A/Gene: gag-akt
 C/Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase
 F/1-129/Product: core protein p15 #status predicted <CP1>
 F/130-214/Product: inner coat protein p12 #status predicted <CP2>
 F/284-763/Product: kinase-related transforming protein akt #status predicted <AKT>
 F/287-389/Domain: pleckstrin repeat homology <PLK>
 F/431-691/Domain: protein kinase homology <KIN>
 F/439-447/Region: protein kinase ATP-binding motif
 F/25,337/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/462/Active site: Lys #status predicted
 F/609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 763;
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPOFSY 6
 Db 752 PPOFSY 757

RESULT 10

T40280
 26S proteasome regulatory complex chain mts3 [validated] - fission yeast (Schizosaccharon
 N/Alternate names: 26S proteasome regulatory complex chain p31 homolog
 C/Species: Schizosaccharomyces pombe
 C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
 C/Accession: T40280; T39593; T52531
 R/McDougal, R.; Rajandream, M.A.; Barrell, B.G.; Saunders, D.; Quail, M.; Harris, D.
 submitted to the EMBL Data Library, July 1999
 A/Reference number: Z21917
 A/Accession: T40280
 A/Molecule type: DNA
 A/Residues: 1-159 <MCD>
 A/Cross-references: UNIPROT:P50524; UNIPARC:UPI000016210B; EMBL:AL096809; PIDN:CA846777.1
 R/Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
 submitted to the EMBL Data Library, May 1998
 A/Reference number: Z21866
 A/Accession: T39593
 A/Molecule type: DNA
 A/Residues: 127-270 <LYN>
 A/Cross-references: UNIPARC:UPI0000169070; EMBL:AL023554; PIDN:CAA19021.1; GSPDB:GN00067;
 R/Gordon, C.; McGurk, G.; Wallace, M.; Hastie, N.D.
 J. Biol. Chem. 271, 5704-5711, 1996
 A/Title: A conditional lethal mutation in the fission yeast 26S protease subunit mts3+ is c
 A/Reference number: Z26102
 A/Accession: T52531
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-270 <GOR>
 A/Cross-references: UNIPARC:UPI000012F86D; EMBL:X92682; PIDN:CAA63366.1
 C/Genetics:
 A/Gene: mts3
 C/Function:
 A/Description: responsible for transition from metaphase to anaphase [validated, MUID:96;
 C/Superfamily: human 26S proteasome regulatory complex chain p31
 C/Keywords: proteasome; protein degradation

Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 270;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 Db 157 PPOFSY 162

RESULT 11

T39064
 RNA binding protein - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T39064
 R/Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, V.
 submitted to the EMBL Data Library, August 1997
 A/Reference number: Z21825
 A/Accession: T39064
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-655 <MUR>
 A/Cross-references: UNIPROT:Q92347; UNIPARC:UPI000013A99A; EMBL:Z61317; PIDN:CAB03604.1;
 A/Experimental source: strain 972h-; cosmid c6G9
 C/Genetics:
 A/Gene: SPDB:SPAC6G9.02C
 A/Map position: 1

Query Match 91.4%; Score 32; DB 2; Length 655;

Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 246 FPOFAY 251

RESULT 12

B71128

probable iron (III) dicitrate transport ATP-binding protein - *Pyrococcus horikoshii*
C/Species: *Pyrococcus horikoshii*
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004

C/Accession: B71128

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Onifuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A/Reference number: A71000; PMID:98344137; PMID:9679194

A/Accession: B71128

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-241 <RAW>

A/Cross-references: UNIPROT:O58521; UNIPARC:UPI00006680B; GB:AP000003; NID:G3236130; PI
A/Experimental source: strain OT3

A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:

A/Gene: PH0791

C/Keywords: ATP
F/21-204/Domain: ATP-binding cassette homology <ABC>

Query Match

Best Local Similarity 88.6%; Score 31; DB 2; Length 241;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 88 FPOFSF 93

RESULT 13

H35068

apolipoprotein H-related protein 23L1 - mouse
C/Species: *Mus musculus* (house mouse)

C/Date: 27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: H35068; A35069; B35069; I35068

R;Vik, D.P.; Munoz-Canoves, P.; Kozono, H.; Martin, L.G.; Tack, B.F.; Chaplin, D.D.
J. Biol. Chem. 265, 3193-3201, 1990

A/Title: Identification and sequence analysis of four complement factor H-related trans
A/Reference number: A35070; PMID:90153965; PMID:1689298

A/Accession: H35068

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-303 <VIK>
A/Cross-references: UNIPROT:O61405; UNIPARC:UPI0000248DB; GB:M29007; NID:G192557; PIDN:
C/Note: translation of the nucleotide sequence is not complete

C/Superfamily: complement C3d/Bpstein-Barr virus receptor; complement factor H repeat ho
C/Keywords: duplication

F/28-81/Domain: complement factor H repeat homology <FH01>
F/86-146/Domain: complement factor H repeat homology <FH02>

F/150-203/Domain: complement factor H repeat homology <FH03>
F/212-266/Domain: complement factor H repeat homology <FH04>

Query Match

Best Local Similarity 88.6%; Score 31; DB 2; Length 303;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 88 FPOFSY 93

RESULT 14

MFNZFU
matrix protein - Sendai virus (strain Fushimi)

C/Species: Sendai virus
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S10330

R;Willenbrink, W.; Neubert, W.J.
Nucleic Acids Res. 18, 3993, 1990

A/Title: Cloning and sequencing of the matrix protein gene (M) of Sendai virus (strain F
A/Reference number: S10330; PMID:90326529; PMID:2165255

A/Accession: S10330
A/Molecule type: genomic RNA

A/Residues: 1-348 <WIL>
A/Cross-references: UNIPROT:P17748; UNIPARC:UPI000013897A; GB:X53056; NID:G62017; PIDN:C/

A/Experimental source: ATCC VR-105
C/Genetics:

A/Gene: M
C/Superfamily: parainfluenza virus matrix protein
C/Keywords: matrix protein

Query Match

Best Local Similarity 88.6%; Score 31; DB 1; Length 348;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 7 FPKFSY 12

RESULT 15

MFNZS

matrix protein - Sendai virus (strain Harliss)

C/Species: Sendai virus
C/Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C/Accession: A04042

R;Blumberg, B.M.; Rose, K.; Simona, M.G.; Roux, L.; Giorgi, C.; Kolakofsky, D.
J. Virol. 52, 656-663, 1984

A/Title: Analysis of the Sendai virus M gene and protein.
A/Reference number: A04042; PMID:85033911; PMID:6092688

A/Accession: A04042
A/Molecule type: genomic RNA

A/Residues: 1-348 <BLU>
A/Cross-references: UNIPROT:P03426; UNIPARC:UPI000013897B; GB:K02742; NID:G334935; PIDN:J

C/Superfamily: parainfluenza virus matrix protein
C/Keywords:

Query Match

Best Local Similarity 88.6%; Score 31; DB 1; Length 348;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPOFSY 6
Db 7 FPKFSY 12

Search completed: June 14, 2006, 02:17:20
Job time : 25 secs

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:59 ; Search time 9.5 Seconds
(without alignments)
7.985 Million cell updates/sec

Title: 09937009-A

Perfect score: 36

Sequence: 1 firstdy 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*
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2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB.pep:*
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8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	91.7	463	US-10-953-349-2983	Sequence 2983, Ap
2	33	91.7	464	US-10-953-349-2982	Sequence 2982, Ap
3	33	91.7	483	US-10-953-349-2981	Sequence 2981, Ap
4	32	88.9	163	US-11-293-697-2752	Sequence 2752, Ap
5	31	86.1	247	US-10-511-937-2422	Sequence 2422, Ap
6	31	86.1	1924	US-10-512-386-56	Sequence 56, Appl
7	30	83.3	292	US-10-953-349-7286	Sequence 7286, Ap
8	30	83.3	300	US-10-953-349-7285	Sequence 7285, Ap
9	30	83.3	402	US-10-953-349-7284	Sequence 7284, Ap
10	30	83.3	429	US-10-953-349-7283	Sequence 7283, Ap
11	29	80.6	197	US-10-953-349-23710	Sequence 23710, A
12	29	80.6	511	US-11-316-521-31	Sequence 31, Appl
13	29	80.6	525	US-11-313-836-10	Sequence 10, Appl
14	29	80.6	571	US-10-953-349-31976	Sequence 31976, A
15	29	80.6	640	US-10-953-349-31975	Sequence 31975, A
16	29	80.6	669	US-10-953-349-31974	Sequence 31974, A
17	28	77.8	271	US-10-953-349-12760	Sequence 12760, A
18	28	77.8	280	US-11-293-697-3893	Sequence 3893, Ap
19	28	77.8	485	US-10-953-349-12759	Sequence 12759, A
20	28	77.8	4051	US-10-501-834-7	Sequence 7, Appli
21	28	77.8	4059	US-10-501-834-6	Sequence 6, Appli
22	28	77.8	4074	US-10-501-834-2	Sequence 2, Appli
23	27	75.0	118	US-10-506-063A-6	Sequence 6, Appli
24	27	75.0	256	US-10-953-349-19900	Sequence 19900, A
25	27	75.0	300	US-10-953-349-19899	Sequence 19899, A

26	27	75.0	340	US-10-953-349-17750	Sequence 17750, A
27	27	75.0	418	US-10-953-349-17749	Sequence 17749, A
28	27	75.0	439	US-10-953-349-19898	Sequence 19898, A
29	27	75.0	439	US-11-181-115-33	Sequence 33, Appl
30	27	75.0	439	US-11-181-115-45	Sequence 45, Appl
31	27	75.0	479	US-10-953-349-17748	Sequence 17748, A
32	27	75.0	488	US-11-317-983-5	Sequence 5, Appli
33	27	75.0	498	US-11-317-983-4	Sequence 4, Appli
34	27	75.0	530	US-10-471-571A-2082	Sequence 2082, Ap
35	26	72.2	104	US-10-953-349-39811	Sequence 39811, A
36	26	72.2	112	US-10-953-349-34760	Sequence 34760, A
37	26	72.2	129	US-10-370-959-130	Sequence 130, App
38	26	72.2	163	US-10-953-349-28654	Sequence 28654, A
39	26	72.2	195	US-10-953-349-28653	Sequence 28653, A
40	26	72.2	234	US-10-471-571A-3990	Sequence 3990, Ap
41	26	72.2	268	US-10-953-349-25610	Sequence 25610, A
42	26	72.2	296	US-10-953-349-25609	Sequence 25609, A
43	26	72.2	303	US-10-953-349-31752	Sequence 31752, A
44	26	72.2	339	US-10-953-349-31751	Sequence 31751, A
45	26	72.2	675	US-11-293-697-3326	Sequence 3326, Ap

ALIGNMENTS

RESULT 1
US-10-953-349-2983
; Sequence 2983, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2983
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2983
; Sequence 2982, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2982
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2982
Query Match 91.7%; Score 33; DB 6; Length 463;
Best Local Similarity 83.3%; Pred. NO. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 FRDPDY 6
Db 319 FKDPDY 324
RESULT 2
US-10-953-349-2982
; Sequence 2982, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2982
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2982
Query Match 91.7%; Score 33; DB 6; Length 464;

Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 320 FKDFDY 325

RESULT 3

US-10-953-349-2981
; Sequence 2281, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2981
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2981

Query Match 91.7%; Score 33; DB 6; Length 483;
Best Local Similarity 83.3%; Pred. No. 9.7;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 339 FKDFDY 344

RESULT 4

US-11-293-697-2752
; Sequence 2752, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2752
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2752

Query Match 88.9%; Score 32; DB 7; Length 163;
Best Local Similarity 83.3%; Pred. No. 4.8;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 149 FRDFDY 154

RESULT 5

US-10-511-937-2422
; Sequence 2422, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2422
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2422

Query Match 86.1%; Score 31; DB 6; Length 247;
Best Local Similarity 83.3%; Pred. No. 12;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 178 FRDFDY 183

RESULT 6

US-10-512-386-56
; Sequence 56, Application US/10512386
; Publication No. US2006008837A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
; FILE REFERENCE: GFU-A0203Y1P
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4706
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1924
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-512-386-56

Query Match 86.1%; Score 31; DB 6; Length 1924;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 1500 FRDFDY 1505

RESULT 7

US-10-953-349-7286
; Sequence 7286, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES


```

; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7286
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7286

```

```

Query Match      83.3%; Score 30; DB 6; Length 292;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 FRDPDY 6
        |||||
Db      58 FSDFDY 63

```

```

RESULT 8
US-10-953-349-35355
; Sequence 35355, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35355
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35355

```

```

Query Match      83.3%; Score 30; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 RDPDY 6
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Db      218 RDPDY 222

```

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RESULT 9
US-10-953-349-7285
; Sequence 7285, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7285
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7285

```

```

Query Match      83.3%; Score 30; DB 6; Length 402;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 FRDPDY 6

```

```

Db      168 FSDFDY 173

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RESULT 10
US-10-953-349-7284
; Sequence 7284, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7284
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7284

```

```

Query Match      83.3%; Score 30; DB 6; Length 429;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 FRDPDY 6
        |||||
Db      195 FSDFDY 200

```

```

RESULT 11
US-10-953-349-23710
; Sequence 23710, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23710
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23710

```

```

Query Match      80.6%; Score 29; DB 6; Length 197;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 FRDPDY 6
        |||||
Db      4 FLDPDY 9

```

```

RESULT 12
US-11-316-521-31
; Sequence 31, Application US/11316521
; Publication No. US2006011848A1
; GENERAL INFORMATION:
; APPLICANT: Carlow, Clotilde K.S.
; APPLICANT: Foster, Jeremy
; APPLICANT: Zhang, Yinhua
; APPLICANT: Kumar, Sanjay
; TITLE OF INVENTION: Identification and Use of Cofactor Independent Phosphoglycerate
; TITLE OF INVENTION: Mutase as a Drug Target for Pathogenic Organisms and Treatment c
; FILE REFERENCE: NEB-230-PCIP-US

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;; CURRENT APPLICATION NUMBER: US/11/316,521
;; CURRENT FILING DATE: 2005-12-22
;; PRIOR APPLICATION NUMBER: US 60/483,566
;; PRIOR FILING DATE: 2003-06-27
;; PRIOR APPLICATION NUMBER: PCT/US2004/018200
;; PRIOR FILING DATE: 2004-06-04
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 31
;; LENGTH: 511
;; TYPE: PRT
;; ORGANISM: Bacillus subtilis
US-11-316-521-31

Query Match 80.6%; Score 29; DB 7; Length 511;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPD 5
Db 277 FRDPD 281

RESULT 13
US-11-313-836-10
; Sequence 10, Application US/11313836
; Publication No. US20060116508A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsai, Fong-ying
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SCL, NARC 10A, NARC 10A, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; FILE REFERENCE: MP103-0620NMIM
; CURRENT APPLICATION NUMBER: US/11/313, 836
; CURRENT FILING DATE: 2005-12-21
; PRIOR APPLICATION NUMBER: US/10/426, 776
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229, 662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795, 691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185, 517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105, 992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406, 045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314, 881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773, 426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495, 823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692, 785
; PRIOR FILING DATE: 2000-10-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 525

;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-11-313-836-10

Query Match 80.6%; Score 29; DB 7; Length 525;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 150 FRDPDY 155

RESULT 14
US-10-953-349-31976
; Sequence 31976, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953, 349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31976
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31976

Query Match 80.6%; Score 29; DB 6; Length 571;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 287 FRDPDY 292

RESULT 15
US-10-953-349-31975
; Sequence 31975, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953, 349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31975
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31975

Query Match 80.6%; Score 29; DB 6; Length 640;
Best Local Similarity 83.3%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 356 FRDPDY 361

Search completed: June 14, 2006, 02:38:21
Job time : 9.5 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:29 ; Search time 124.5 Seconds
(Without alignments)
22.324 Million cell updates/sec

Title: 09937009-A

Sequence: 36

Scoring table: 1 firstdy 6

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	4	US-10-148-786A-55
2	36	100.0	6	4	US-10-217-574-9
3	36	100.0	6	4	US-10-217-555-8
4	36	100.0	11	4	US-10-217-574-25
5	36	100.0	11	4	US-10-217-555-25
6	36	100.0	15	4	US-10-217-574-4
7	36	100.0	23	4	US-10-148-786A-5
8	36	100.0	23	4	US-10-217-574-23
9	36	100.0	23	4	US-10-217-555-23
10	36	100.0	24	4	US-10-148-786A-22
11	36	100.0	24	4	US-10-217-574-12
12	36	100.0	24	4	US-10-217-555-11
13	36	100.0	35	4	US-10-380-235-33
14	36	100.0	35	4	US-10-380-235-35
15	36	100.0	39	4	US-10-148-786A-3
16	36	100.0	39	4	US-10-148-786A-34
17	36	100.0	39	5	US-10-994-093-13
18	36	100.0	39	5	US-10-922-337-9
19	36	100.0	39	6	US-11-192-341-3
20	36	100.0	77	4	US-10-148-786A-8
21	36	100.0	334	4	US-10-217-574-18
22	36	100.0	334	4	US-10-217-555-18
23	36	100.0	725	5	US-10-491-467-45
24	36	100.0	786	3	US-09-950-041-2
25	36	100.0	786	3	US-10-732-563-2
26	36	100.0	786	4	US-10-732-796A-2
27	36	100.0	786	5	US-10-491-997-50

28	36	100.0	786	5	US-10-975-909-2	Sequence 2, Appl1
29	36	100.0	984	4	US-10-029-905-10	Sequence 106, Appl
30	36	100.0	984	4	US-10-354-358-106	Sequence 106, App
31	33	91.7	224	3	US-09-882-227-100	Sequence 5500, Ap
32	33	91.7	235	4	US-10-335-977-5500	Sequence 5501, Ap
33	33	91.7	236	4	US-10-335-977-5501	Sequence 5990, Ap
34	33	91.7	329	5	US-10-501-282-5990	Sequence 5993, Ap
35	33	91.7	352	6	US-11-097-143-9603	Sequence 5983, Ap
36	33	91.7	464	5	US-10-739-930-5983	Sequence 106389,
37	33	91.7	940	4	US-10-437-963-106389	Sequence 2, Appl1
38	33	91.7	1390	4	US-10-039-112-2	Sequence 2, Appl1
39	33	91.7	1390	5	US-10-761-983-2	Sequence 15, Appl
40	33	91.7	2237	6	US-11-010-775-15	Sequence 274652,
41	32	88.9	158	4	US-10-424-599-274652	Sequence 2752, Ap
42	32	88.9	163	4	US-10-108-260A-2752	Sequence 691, App
43	32	88.9	169	3	US-09-764-875-691	Sequence 144, App
44	32	88.9	175	3	US-09-764-881-144	Sequence 144, App
45	32	88.9	175	3	US-09-764-881-144	

ALIGNMENTS

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RESULT 1
US-10-148-786A-55
; Sequence 55, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148.786A
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-786A-55

Query Match      100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FRDPDY 6
DB      1 FRDPDY 6

RESULT 2
US-10-217-574-9
; Sequence 9, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217.574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
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/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-574-9
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Query Match          100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY          1 FRDPDY 6
            |||||
Db          1 FRDPDY 6
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RESULT 3
US-10-217-555-8
/ Sequence 8, Application US/10217555
/ Publication No. US20040009569A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
/ FILE REFERENCE: 44236
/ CURRENT APPLICATION NUMBER: US/10/217,555
/ CURRENT FILING DATE: 2002-12-05
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-555-8
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Query Match          100.0%; Score 36; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY          1 FRDPDY 6
            |||||
Db          1 FRDPDY 6
```

```
RESULT 4
US-10-217-574-25
/ Sequence 25, Application US/10217574
/ Publication No. US20040005687A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures
/ FILE REFERENCE: 44237
/ CURRENT APPLICATION NUMBER: US/10/217,574
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: GB 0216215.4
/ PRIOR FILING DATE: 2002-07-12
/ NUMBER OF SEQ ID NOS: 46
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/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-574-25
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Query Match          100.0%; Score 36; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY          1 FRDPDY 6
            |||||
Db          2 FRDPDY 7
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RESULT 5
US-10-217-555-25
/ Sequence 25, Application US/10217555
/ Publication No. US20040009569A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
/ FILE REFERENCE: 44236
/ CURRENT APPLICATION NUMBER: US/10/217,555
/ CURRENT FILING DATE: 2002-12-05
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-555-25
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```
Query Match          100.0%; Score 36; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY          1 FRDPDY 6
            |||||
Db          2 FRDPDY 7
```

```
RESULT 6
US-10-217-574-4
/ Sequence 4, Application US/10217574
/ Publication No. US20040005687A1
/ GENERAL INFORMATION:
/ APPLICANT: Barford, David
/ APPLICANT: Yang, Jing
/ APPLICANT: Hemmings, Brian A
/ APPLICANT: Cron, Peter D
/ TITLE OF INVENTION: Kinase Crystal Structures
/ FILE REFERENCE: 44237
/ CURRENT APPLICATION NUMBER: US/10/217,574
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: GB 0119860.5
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: GB 0209985.1
/ PRIOR FILING DATE: 2002-05-01
/ PRIOR APPLICATION NUMBER: GB 0216215.4
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;; PRIOR FILING DATE: 2002-07-12
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C-terminal
;; OTHER INFORMATION: tail
US-10-217-574-4

Query Match 100.0%; Score 36; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 6 FRDPDY 11

RESULT 7
US-10-148-786A-5
; Sequence 5, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-5

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 13 FRDPDY 18

RESULT 8
US-10-217-574-23
; Sequence 23, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

;; LENGTH: 23
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-574-23

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 14 FRDPDY 19

RESULT 9
US-10-217-555-23
; Sequence 23, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-217-555-23

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 14 FRDPDY 19

RESULT 10
US-10-148-786A-22
; Sequence 22, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleesi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-10-148-786A-22

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 11
US-10-217-574-12

; Sequence 12, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 020985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-574-12

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 12
US-10-217-555-11

; Sequence 11, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 020985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-217-555-11

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 13
US-10-380-235-33

; Sequence 33, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:
; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,423
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/238,558
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-235-33

Query Match 100.0%; Score 36; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 29 FRDPDY 34

RESULT 14
US-10-380-235-35

; Sequence 35, Application US/10380235
; Publication No. US20040072184A1
; GENERAL INFORMATION:
; APPLICANT: Yoganathan, Thillainathan
; APPLICANT: Delaney, Allen
; TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: KINE-024CIP
; CURRENT APPLICATION NUMBER: US/10/380,235
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: IB01/02237
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/290,555
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/233,999
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 60/237,423
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/238,558
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 35
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens
US-10-380-235-35

Query Match 100.0%; Score 36; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
|||
Db 29 FRDFDY 34

RESULT 15
US-10-148-786A-3
Sequence 3, Application US/10148786A
Publication No. US20030143656A1
GENERAL INFORMATION:
APPLICANT: Aleasi, Dario
APPLICANT: Biondi, Riccardo
TITLE OF INVENTION: Protein Kinase Regulation
FILE REFERENCE: 002.00210
CURRENT APPLICATION NUMBER: US/10/148,786A
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 3
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-3

Query Match 100.0%; Score 36; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
|||
Db 29 FRDFDY 34

Search completed: June 14, 2006, 02:37:57
Job time : 125.5 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2006, 02:16:55 ; Search time 38 Seconds
(without alignments)
13.821 Million cell updates/sec

Title: 09937009-A
Perfect score: 36
Sequence: 1 frdfdy 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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4: /EMC_Celerra_SIDS3/prodata/2/iaa/H COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCTUS COMB.pep:*
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7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	36	100.0	672	2	US-09-949-002-522
2	36	100.0	786	2	US-09-949-002-351
3	36	100.0	1041	2	US-09-949-016-7878
4	33	91.7	176	2	US-09-248-796A-18362
5	33	91.7	209	2	US-09-270-767-41925
6	33	91.7	993	1	US-08-836-687B-30
7	33	91.7	1390	1	US-08-770-544-2
8	33	91.7	1390	2	US-09-579-259-2
9	33	91.7	1390	2	US-09-650-324A-2
10	33	91.7	1390	2	US-10-039-112A-2
11	32	88.9	144	2	US-09-513-999C-7038
12	32	88.9	345	2	US-09-248-796A-20158
13	31	86.1	226	1	US-07-929-198-2
14	31	86.1	226	1	US-07-929-198-4
15	31	86.1	226	1	US-07-929-198-6
16	31	86.1	226	1	US-08-557-146-15
17	31	86.1	226	1	US-09-154-344-15
18	31	86.1	226	1	US-08-944-483-43
19	31	86.1	1924	3	US-09-866-557A-2
20	30	83.3	118	2	US-09-254-180C-3
21	30	83.3	118	2	US-09-065-059-5
22	30	83.3	118	2	US-08-913-555-5
23	30	83.3	119	2	US-09-254-180C-16
24	30	83.3	119	2	US-09-254-180C-18
25	30	83.3	119	2	US-09-254-180C-19
26	30	83.3	119	2	US-09-254-180C-149

27	30	83.3	119	2	US-08-913-555-23	Sequence 23, App1
28	30	83.3	138	2	US-09-254-180C-143	Sequence 143, App
29	30	83.3	219	2	US-09-254-180C-180	Sequence 180, App
30	30	83.3	281	2	US-09-605-703B-114	Sequence 114, App
31	30	83.3	281	2	US-09-605-703B-116	Sequence 116, App
32	30	83.3	718	2	US-09-252-991A-28229	Sequence 28229, A
33	30	83.3	789	2	US-09-712-363-244	Sequence 244, App
34	29	80.6	85	2	US-09-621-976-4345	Sequence 4345, App
35	29	80.6	124	2	US-09-270-767-33226	Sequence 33226, A
36	29	80.6	124	2	US-09-270-767-48443	Sequence 48443, A
37	29	80.6	136	2	US-09-270-767-32985	Sequence 32985, A
38	29	80.6	136	2	US-09-270-767-48202	Sequence 48202, A
39	29	80.6	147	2	US-09-270-767-31908	Sequence 31908, A
40	29	80.6	147	2	US-09-270-767-33287	Sequence 33287, A
41	29	80.6	147	2	US-09-270-767-47125	Sequence 47125, A
42	29	80.6	147	2	US-09-270-767-48504	Sequence 48504, A
43	29	80.6	148	2	US-09-640-211A-787	Sequence 787, App
44	29	80.6	151	2	US-09-270-767-32172	Sequence 32172, A
45	29	80.6	151	2	US-09-270-767-33218	Sequence 33218, A

ALIGNMENTS

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RESULT 1
US-09-949-002-522
; Sequence 522, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 522
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-522

Query Match      100.0%; Score 36; DB 2; Length 672;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FRDFDY 6
Db      175 FRDFDY 180

RESULT 2
US-09-949-002-351
; Sequence 351, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 786

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TYPE: PRT
ORGANISM: Human
US-09-949-002-351

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 786;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 289 FRDFDY 294

RESULT 3
US-09-949-016-7878
Sequence 7878, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7878

LENGTH: 1041

TYPE: PRT

ORGANISM: Human

US-09-949-016-7878

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 1041;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 1031 FRDFDY 1036

RESULT 4
US-09-248-796A-18362

Sequence 18362, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18362

LENGTH: 176

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-18362

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 176;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 97 FRDFDY 102

RESULT 5
US-09-270-767-41925
Sequence 41925, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 41925

LENGTH: 209

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-41925

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 209;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 128 FRDFDY 133

RESULT 6
US-08-836-687B-30

Sequence 30, Application US/08836687B

Patent No. 6448034

GENERAL INFORMATION:

APPLICANT: Gasson, Michael John

APPLICANT: Dodd, Helen Maix

TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN

FILE REFERENCE: 20747/70

CURRENT APPLICATION NUMBER: US/08/836,687B

CURRENT FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 993

TYPE: PRT

ORGANISM: Lactococcus sp.

US-08-836-687B-30

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 993;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 595 FRDFDY 600

RESULT 7
US-08-770-544-2
Sequence 2, Application US/08770544

Patent No. 5907085

GENERAL INFORMATION:

APPLICANT: Gonsalves, Dennis

APPLICANT: Ling, Kai-Shu

TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND

TITLE OF INVENTION: THEIR USES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1390 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-770-544-2

Query Match 91.7%; Score 33; DB 1; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
:|||||
Db 421 YRDPDY 426

RESULT 8
US-09-579-259-2
Sequence 2, Application US/09579259
Patent No. 6558953
GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
LING, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS
PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/579,259
FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60009008
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1390 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-579-259-2

Query Match 91.7%; Score 33; DB 2; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
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Db 421 YRDPDY 426

RESULT 9
US-09-650-324A-2
Sequence 2, Application US/09650324A
Patent No. 6638720
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
LING, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
THEIR USES
FILE REFERENCE: 07678/025006
CURRENT APPLICATION NUMBER: US/09/650,324A
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 09/579,259
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/224,898
PRIOR FILING DATE: 1998-12-31
PRIOR APPLICATION NUMBER: US 08/770,544
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: US 60/009,008
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1390
TYPE: PRT
ORGANISM: Grapevine leafroll virus
US-09-650-324A-2

Query Match 91.7%; Score 33; DB 2; Length 1390;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
:|||||
Db 421 YRDPDY 426

RESULT 10
US-10-039-112A-2
Sequence 2, Application US/10039112A
Patent No. 6916617
GENERAL INFORMATION:
APPLICANT: GONSALVES, DENNIS
LING, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
THEIR USES
FILE REFERENCE: 07678/025007
CURRENT APPLICATION NUMBER: US/10/039,112A
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 09/650,324

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; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 09/579,259
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/224,898
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 08/770,544
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/009,008
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1390
; TYPE: PRT
; ORGANISM: Grapevine leafroll virus
US-10-039-112A-2

Query Match
Best Local Similarity 91.7%; Score 33; DB 2; Length 1390;
Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 421 YRDPDY 426

RESULT 11
US-09-513-999C-7038
; Sequence 7038, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 7038
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: UNSURE
; LOCATION: 103
; OTHER INFORMATION: Xaa=Glu or Gly
US-09-513-999C-7038

Query Match
Best Local Similarity 88.9%; Score 32; DB 2; Length 114;
Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 13 FRDPDY 18

RESULT 12
US-09-248-796A-20158
; Sequence 20158, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
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; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 20158
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20158

Query Match
Best Local Similarity 88.9%; Score 32; DB 2; Length 345;
Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 7 FRDPDY 12

RESULT 13
US-07-929-198-2
; Sequence 2, Application US/07929198
; Patent No. 5567602
; GENERAL INFORMATION:
; APPLICANT: Clark, James M.
; APPLICANT: Shoemaker, Kevin R.
; APPLICANT: Warne, Robert L.
; TITLE OF INVENTION: Recombinant Production of Chymase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/929,198
; FILING DATE: 19920812
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7056-017-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-929-198-2

Query Match
Best Local Similarity 86.1%; Score 31; DB 1; Length 226;
Matches 5; Conservativity 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
Db 157 FRDPDY 162

RESULT 14
US-07-929-198-4
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Sequence 4, Application US/07929198
Patent No. 5567602
GENERAL INFORMATION:
APPLICANT: Clark, James M.
APPLICANT: Shoemaker, Kevin R.
APPLICANT: Warne, Robert L.
TITLE OF INVENTION: Recombinant Production of Chymase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,198
FILING DATE: 19920812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7056-017-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-929-198-4

Query Match 86.1%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 157 FRDPDH 162

RESULT 15
US-07-929-198-6
Sequence 6, Application US/07929198
Patent No. 5567602
GENERAL INFORMATION:
APPLICANT: Clark, James M.
APPLICANT: Shoemaker, Kevin R.
APPLICANT: Warne, Robert L.
TITLE OF INVENTION: Recombinant Production of Chymase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,198

FILING DATE: 19920812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7056-017-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-929-198-6

Query Match 86.1%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDPDY 6
Db 157 FRDPDH 162

Search completed: June 14, 2006, 02:18:39
Job time : 39 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:38 ; Search time 154.5 Seconds
(without alignments)
17.756 Million cell updates/sec

Title: 00937009-A
Perfect score: 36
Sequence: 1 fxdidy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	6	ABR57448	Abi57448 PKB activ
2	36	100.0	6	ADJ38853	Adj38853 PKR2 AGC
3	36	100.0	11	ABR57456	Abi57456 Protein k
4	36	100.0	11	ADB92666	Adb92666 Peptide p
5	36	100.0	11	ADV91663	Adv91663 Activated
6	36	100.0	15	ADB92676	Adb92676 Crystalli
7	36	100.0	23	AA898805	Aa898805 3-phospho
8	36	100.0	23	ABR57454	Abi57454 Protein k
9	36	100.0	23	ADB92664	Adb92664 Peptide p
10	36	100.0	23	ADV91662	Adv91662 Activated
11	36	100.0	24	AA947729	Aa947729 Region B
12	36	100.0	24	AA947726	Aa947726 Peptide c
13	36	100.0	24	AA899799	Aa899799 Protein k
14	36	100.0	24	AA899794	Aa899794 3-phospho
15	36	100.0	24	ABR57451	Abi57451 PKB activ
16	36	100.0	25	ADY20891	Ady20891 PDK1-inte
17	36	100.0	35	AAE22774	Aae22774 Human SGK
18	36	100.0	39	AA898812	Aa898812 PDK1 pept
19	36	100.0	39	AA898806	Aa898806 3-phospho
20	36	100.0	39	ADJ38899	Adj38899 PDK1-tide
21	36	100.0	39	AD043310	Ado43310 Human PDK
22	36	100.0	39	ADR23147	Adr23147 Human sub
23	36	100.0	39	ADT07106	Adt07106 3'-phosph

24	36	100.0	39	ADV67122	Adv67122 3'-phosph
25	36	100.0	39	ADW86518	Adw86518 Substrate
26	36	100.0	39	AD874403	Ad874403 PKRtide p
27	36	100.0	39	ABE17979	Aeb17979 Peptide u
28	36	100.0	39	ABE97117	Aee97117 Human kin
29	36	100.0	39	ABE68515	Aee68515 3-phospho
30	36	100.0	77	AA899793	Aa899793 3-phospho
31	36	100.0	91	ADY20895	Ady20895 PDK-1 inh
32	36	100.0	91	ADY20892	Ady20892 PDK-1 inh
33	36	100.0	315	AA899835	Aa899835 AGC prote
34	36	100.0	315	ADJ38883	Adj38883 PKR2 amin
35	36	100.0	334	ABR57466	Abi57466 AGC famil
36	36	100.0	343	ADY20896	Ady20896 PDK-1 inh
37	36	100.0	345	ADY20894	Ady20894 GFP-conju
38	36	100.0	385	AA899822	Aa899822 AGC prote
39	36	100.0	725	ADC99092	Adc99092 Human KPP
40	36	100.0	786	AA866349	Aa866349 Human DNA
41	36	100.0	786	AAE16090	Aae16090 Human DNA
42	36	100.0	786	ADC78821	Adc78821 Human PRO
43	36	100.0	786	ADE25535	Ade25535 Human rel
44	36	100.0	786	ADP56650	Adp56650 Human Tol
45	36	100.0	786	ADP48591	Adp48591 Human Tol

ALIGNMENTS

RESULT 1
ID ABR57448 standard; peptide; 6 AA.
XX ABR57448;
AC
XX
DT 15-SEP-2003 (first entry)
XX
XX PKB activity modulating peptide #12.
DE
XX
XX Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
KW protein co-ordinate data; cytosolic; antidiabetic; vasotropic; PKB;
KW neurotrophic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
KW structural analysis; cancer; diabetes; erectile dysfunction;
KW neurodegeneration.
XX
XX Synthetic.
OS
XX
XX WO2003016516-A2.
PN
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-GB003735.
XX
XX 14-AUG-2001; 2001GB-00019860.
PR 01-MAY-2002; 2002GB-00009985.
XX
XX (NOVS) NOVARTIS FORSCHUNGSSITFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD;
PI WPI; 2003-268328/26.
XX
XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX Claim 32; Page 265; 284pp; English.
XX
XX The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space
CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =

CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC a = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cytostatic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which can be used in a method from the present invention to
CC modulate PKB activity

XX Sequence 6 AA;
XX

Query Match	100.0%;	Score 36;	DB 6;	Length 6;
Similarity	100.0%;	Pred. No. 2.1e+06;		
Matches	6;	Conservative	0;	Indels 0;
				Gaps 0;

QY	1	FR	DE	DY	6
nb	1	FR	DE	DY	6

```

RESULT 2
ADJ38853
ID ADJ38853 standard; peptide; 6 AA.

```

AC ADJ38853;

DT 06-MAY-2004 (first entry)

DE PRK2 AGC hydrophobic motif peptide.

KW phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;

insulin signalling pathway; signalling; crystalline form;

KW antidiabetic; cardiant; cytostatic; cerebroprotective; va

KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;

XX

XX

XX

XX

XX

XXXX

XX

XX

XX

PT dependent protein kinase 1 by using molecular modelling to select/design

XX

XX

CC a compound for modulating the activity of phosphoinositide dependent

CC select or design a compound that is predicted to interact with the

CC predicted to interact with the protein kinase catalytic domain. Also

described: (1) selecting or designing (M2) a compound for modulating the activity of a hydrophobic pocket (PIF binding pocket)-containing protein kinase having a hydrophobic pocket in the position equivalent to the hydrophobic pocket of human PDK1 that is defined by residues including Lys15, Ile18, Ile19, Val124, Val127 and/or Leu155 of full-length human PDK1 and further having a phosphate binding pocket in the position equivalent to the phosphate binding pocket of human PDK1 that is defined by residues including Lys76, Arg11, Thr148 and/or Glu150; (2) assessing (M3) the activation state of a structure for a protein kinase; (3) a mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a host cell (III) comprising (II); (6) identifying (M4) a compound that modulates the protein kinase activity of a protein kinase (e.g., PDK1); (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1 or (I) or an antibody reactive with PDK1 or (I) but not with the protein kinase mutated at the phosphate binding site, or vice versa; (8) a compound (V) identified or identifiable by (M1) or (M3); (9) use of (V), (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of a medicament for the treatment of a patient in need of modulation of signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or p70 S6 kinase, for example insulin signalling pathway and/or PDK1/PDK2/SGK/p70 S6 kinase/PDK2/PKC signalling; and (11) a crystalline form (VI) of polypeptide as defined in (M1). (I) has antifungal, antidiabetic, cardiac, cytostatic, cerebroprotective, vasotropic and anorectic activities, and can be used as a modulator of protein kinase. (V) is useful for modulating the ability of protein kinase to phosphorylate different substrates, e.g., different naturally occurring polypeptides, to different extents. (V) inhibits or increases the activity of protein kinase. The protein structures e.g., the co-ordinates as provided in the specification are useful for designing reagent useful in drug designing assays or characterisation of protein kinase activity or regulation. (V) capable of producing the activity of PKC, e.g., PKC beta, PRK1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is useful in treating cancer. (V) capable of increasing the activity of PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity or may be useful in inhibiting apoptosis, thus useful in treating diseases in which apoptosis is involved e.g., mechanical (including heart) tissue injury or ischaemia disease such as stroke, myocardial infarction and neural injury. (V) is useful as an antiungal agent. The present sequence is used in the exemplification of the present invention.

Sequence 6 AA;
SQ

Query Match	100.0%;	Score 36;	DB 8;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 2.1e+06;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0.7;

Qy	1	FRDFDY	6
Db	1	FRDFDY	6

RESULT 3
ABR57456
ID ABR57456 standard; peptide; 11 AA.

AC ABR57456;

DT 15-SEP-2003 (first entry)

DE Protein kinase B assay related peptide P1ftidel.

KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;

KW nootropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;

KW neurodegeneration.

OS Synthetic

PN W02003016516-A2.

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002MO-GB003735.
XX
PR 14-AUG-2001; 2001GB-00019860.
PR 01-MAY-2002; 2002GB-00009985.
XX
XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX
PI Barford D, Yang J, Hemmings BA, Cron PD;
XX WPI; 2003-268329/26.
XX
DR
XX
XX
PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX
PS Disclosure; Page 86; 284pp; English.
XX
CC The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space
CC group P4₁-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (II) has cytoskeletal, antidiabetic, vasotropic,
CC nootropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which is used in the exemplification of the present invention
XX
SQ Sequence 11 AA;
XX
Query Match 100.0%; Score 36; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 2 FRDPDY 7
XX
RESULT 4
ADB92666
ID ADB92666 standard; peptide; 11 AA.
XX
XX ADB92666;
XX
XX 01-JAN-2004 (first entry)
DT
XX Peptide PIFcidel.
DE
XX
XX Protein kinase Bbeta; PKBbeta; cytoskeletal; antidiabetic; vasotropic;
KW nootropic; neuroprotective; gene therapy; cancer; diabetes;
KW erectile dysfunction; neurodegeneration; protein co-ordinate data;
KW enzyme; AGC kinase.
XX
XX Synthetic.
OS
XX
XX WO2003016517-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002MO-GB003737.
PF
XX
XX 14-AUG-2001; 2001GB-00019860.
PR

PR 01-MAY-2002; 2002GB-00009985.
PR 12-JUL-2002; 2002GB-00016215.
XX
XX
XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX
XX
PI Barford D, Yang J, Hemmings BA, Cron PD;
XX WPI; 2003-268329/26.
XX
DR
XX
XX
XX
PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX
PS Disclosure; Page 104; 124pp; English.
XX
XX The invention relates to a crystal of protein kinase Bbeta (PKBbeta).
CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancers, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents a peptide used in a
CC protein kinase B assay.
XX
SQ Sequence 11 AA;
XX
Query Match 100.0%; Score 36; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDPDY 6
DB 2 FRDPDY 7
XX
RESULT 5
ADV91663
ID ADV91663 standard; peptide; 11 AA.
XX
XX ADV91663;
XX
XX 24-FEB-2005 (first entry)
DT
XX
XX Activated protein kinase B beta (PKBbeta) peptide, PIFcidel #2.
DE
XX
XX Pharmaceutical; cell signaling; chemotherapy; AGC kinase related disease;
KW cancer; diabetes; neurodegenerative disease; Alzheimers disease;
KW Parkinsons disease; AIDS associated dementia;
KW amyotrophic lateral sclerosis; multiple sclerosis; schizophrenia;
KW scleroderma; cardiomyocyte hypertrophy; reperfusion; ischemia; baldness;
KW neuroprotective; antiparkinsonian; nootropic; anti-hiv; neuroleptic;
KW cardiovascular-gen.; endocrine-gen.; vasotropic; cytoskeletal;
KW antidiabetic; protein kinase B beta; PKBbeta.
XX
XX Unidentified.
OS
XX
XX EPI466488-A1.
PN
XX
XX 15-DEC-2004.
PD
XX
XX 10-JUN-2003; 2003EP-00090177.
PF
XX
XX 10-JUN-2003; 2003EP-00090177.
PR
XX
XX (PHOS-) PHOSPHOSITES GMBH.
PA
XX
XX Blondi R, Engel M;
PI

XX WPI; 2005-041631/05.
XX
XX New ketone, amide, ester and carbonyl derivatives useful for treating
PT e.g. cancer, multiple sclerosis, amyotrophic lateral sclerosis, and
PT Alzheimer's disease, Parkinson's disease, reperfusion, ischemia and
PT diabetes.
XX
XX Disclosure; Page 3; 32pp; English.
XX
XX The present invention relates to small molecules that are protein kinase
CC regulators, activators and inhibitors, compositions containing such
CC compounds and their pharmaceutical use. The invention is useful for the
CC prevention or treatment of a disease related to an AGC kinase such as
CC cancer, diabetes, neurodegenerative diseases, Alzheimer's disease,
CC Parkinson's disease, AIDS associated dementia, amyotrophic lateral
CC sclerosis, multiple sclerosis, schizophrenia, cardiomyocyte hypertrophy,
CC reperfusion, ischemia and baldness. The present sequence is an activated
CC protein kinase B beta (PKBbeta) peptide, Pfifide. PKB belong to the AGC
CC kinase group of enzymes.
XX
XX Sequence 11 AA:

Query Match 100.0%; Score 36; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 2 FRDPDY 7

RESULT 6
ADB92676
ID ADB92676 standard; peptide; 15 AA.
XX
XX ADB92676;

DT 01-JAN-2004 (first entry)
XX

DE Crystallised PKBbeta molecule C-terminal tail.
XX

XX Protein kinase Bbeta; PKBbeta; cytostatic; anti-diabetic; vasotropic;
KM neurotropic; neuroprotective; gene therapy; cancer; diabetes;
KM erectile dysfunction; neurodegeneration; protein co-ordinate data;
XX enzyme; AGC kinase.
XX

OS Unidentified.
XX

PN WO2003016517-A2.
XX

PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-GB003737.
XX

PR 14-AUG-2001; 2001GB-00019860.
XX

PR 01-MAY-2002; 2002GB-0000985.
XX

PR 12-JUL-2002; 2002GB-00016215.
XX

PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
PA (CANC-) CANCER RES INST.
XX

PI Barford D, Yang J, Hemmings BA, Cron PD;
XX

DR WPI; 2003-268329/26.
XX

XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX

PS Claim 6; Page 232; 124pp; English.
XX

XX The invention relates to a crystal of protein kinase Bbeta (PKBbeta).
CC

CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancers, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents the crystallised
CC PKBbeta molecule C-terminal tail.
XX

XX Sequence 15 AA:

Query Match 100.0%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
|||
Db 6 FRDPDY 11

RESULT 7
AAB99805
ID AAB99805 standard; peptide; 23 AA.
XX
XX AAB99805;

DT 20-SEP-2001 (first entry)
XX

DE 3-phosphoinositide-dependent protein kinase 1 interacting peptide #2.
XX

XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;
KM diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.
XX

OS Homo sapiens.
XX

OS Synthetic.
XX

PN WO200144497-A2.
XX

PD 21-JUN-2001.
XX

PD 04-DEC-2000; 2000WO-GB004598.
XX

PF 02-DEC-1999; 99US-0168559P.
XX

PR (UYDU-) UNIV DUNDEE.
XX

PA Alessi D, Blondi R;
XX

PI WPI; 2001-390252/41.
XX

XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides.
XX

PS Claim 14; Page 130; 180pp; English.
XX

XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of a
CC hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
CC polynucleotides from the present invention are useful in medicine,
CC particularly in the manufacture of a medicament for treating a patient in
CC need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is in

CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischemic injury, including stroke. The compound or composition
CC is also useful for inhibiting the degree or rate of phosphorylation by
CC the protein kinase. The interacting polypeptide or compound is useful in
CC methods of stabilizing a hydrophobic pocket-containing protein kinase,
CC where the protein kinase is exposed to the compound or polypeptide.
CC AAB9786 to AAB9847 represent amino acid sequences, and AAH4210 and
CC AAH4211 represent oligonucleotide sequences, used in the exemplification
CC of the present invention

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 36; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6
Db 13 FRDPDY 18

RESULT 8
ABR57454

ID ABR57454 standard; peptide; 23 AA.

XX
AC ABR57454;

DT 15-SEP-2003 (first entry)

DE Protein kinase B assay related peptide P1FtIDE.

XX
KW Protein kinase B: PKB/Akt; enzyme; crystal structure; drug discovery;
KW protein co-ordinate data; cytosolic; antidiabetic; vasotropic; PKB;
KW neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
KW structural analysis; cancer; diabetes; erectile dysfunction;
KW neurodegeneration.

XX
OS Synthetic.

PN WO2003016516-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-GB003735.

PR 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-00009985.

PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
(CANC-) CANCER RES INST.

PI Barford D, Yang J, Hemmings BA, Cron PD;

DR WPI; 2003-268328/26.

PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.

XX
PS Disclosure; Page 86; 284pp; English.

CC The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (1), where (1) comprises: (a) a tetragonal space
CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cytosolic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene

CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancer, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which is used in the exemplification of the present invention

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 36; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FRDPDY 6
Db 14 FRDPDY 19

RESULT 9
ADB92664

ID ADB92664 standard; peptide; 23 AA.

XX
AC ADB92664;

DT 01-JAN-2004 (first entry)

DE Peptide P1FtIDE.

XX
KW Protein kinase Bbeta; PKBbeta; cytosolic; antidiabetic; vasotropic;
KW neurotropic; neuroprotective; gene therapy; cancer; diabetes;
KW erectile dysfunction; neurodegeneration; protein co-ordinate data;
KW enzyme; AGC kinase.

XX
OS Synthetic.

PN WO2003016517-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-GB003737.

PR 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-00009985.

PR 12-JUL-2002; 2002GB-00016215.

PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
(CANC-) CANCER RES INST.

PI Barford D, Yang J, Hemmings BA, Cron PD;

DR WPI; 2003-268329/26.

PT New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.

XX
PS Disclosure; Page 104; 124pp; English.

CC The invention relates to a crystal of protein kinase Bbeta (PKBbeta).
CC Three-dimensional protein coordinate data is given in the specification.
CC Also disclosed is a method for determining the structure of a PKB
CC derivative, analysing a PKBbeta-ligand complex, determining a three-
CC dimensional structure for a target kinase, and a computer system or
CC computer-readable media containing atomic coordinate data listed in the
CC specification. The crystal of PKBbeta, and methods are useful in
CC activating protein kinases, particularly AGC kinases, for identifying
CC modulators of protein kinase activity, and for structural analysis of
CC other protein kinases. The crystal may also be used in manufacturing a
CC medicament for treating cancer, diabetes, erectile dysfunction or
CC neurodegeneration. The current sequence represents a peptide used in a
CC protein kinase B assay.

SQ Sequence 23 AA;
 Query Match 100.0%; Score 36; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRDFDY 6
 Db 14 FRDFDY 19
 RESULT 10
 ADV91662
 ID ADV91662 standard; peptide; 23 AA.
 AC ADV91662;
 XX
 XX 24-FEB-2005 (first entry)
 DE Activated protein kinase B beta (PKBbeta) peptide, Piflide #1.
 XX
 XX Pharmaceutical; cell signaling; chemotherapy; AGC kinase related disease;
 KW cancer; diabetes; neurodegenerative disease; Alzheimers disease;
 KW Parkinsons disease; AIDS associated dementia;
 KW amyotrophic lateral sclerosis; multiple sclerosis; schizophrenia;
 KW scleroderma; cardiomyocyte hypertrophy; reperfusion; ischemia; baldness;
 KW neuroprotective; antiparkinsonian; nootropic; anti-hiv; neuroleptic;
 KW cardiovascular-gen.; endocrine-gen.; vasotropic; cyostatic;
 KM antidiabetic; protein kinase B beta; PKBbeta.
 XX
 XX Unidentified.
 OS
 XX EPI486488-A1.
 PN
 XX 15-DEC-2004.
 PD
 XX 10-JUN-2003; 2003EP-00090177.
 PF
 XX 10-JUN-2003; 2003EP-00090177.
 PR
 XX 10-JUN-2003; 2003EP-00090177.
 PA (PHOS-) PHOSPHOSITES GMBH.
 XX
 PI Biondi R, Engel M;
 XX
 XX WPI; 2005-041631/05.
 DR
 XX New ketone, amide, ester and carbonyl derivatives useful for treating
 PT e.g. cancer, multiple sclerosis, amyotrophic lateral sclerosis,
 PT Alzheimer's disease, Parkinson's disease, reperfusion, ischemia and
 PT diabetes.
 XX
 XX Disclosure; Page 3; 32pp; English.
 PS
 XX The present invention relates to small molecules that are protein kinase
 CC regulators, activators and inhibitors, compositions containing such
 CC compounds and their pharmaceutical use. The invention is useful for the
 CC prevention or treatment of a disease related to an AGC kinase such as
 CC cancer, diabetes, neurodegenerative diseases, Alzheimer's disease,
 CC Parkinson's disease, AIDS associated dementia, amyotrophic lateral
 CC sclerosis, multiple sclerosis, schizophrenia, cardiomyocyte hypertrophy,
 CC reperfusion, ischemia and baldness. The present sequence is an activated
 CC protein kinase B beta (PKBbeta) peptide, Piflide. PKB belong to the AGC
 CC kinase group of enzymes.
 CC
 XX
 SQ Sequence 23 AA;
 Query Match 100.0%; Score 36; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRDFDY 6
 Db 14 FRDFDY 19

RESULT 11
 AA94729
 ID AA94729 standard; peptide; 24 AA.
 AC AA94729;
 XX
 XX 29-JAN-2001 (first entry)
 DT
 XX
 DE Region B of protein kinase C related protein kinase 2.
 XX
 XX Substrate specificity; phosphoinositide-dependent protein kinase 1; PKP1;
 KW protein kinase C related protein kinase 2; PKR2; cancer; apoptosis;
 KW mechanical tissue damage; ischaemic disease; stroke;
 KW myocardial infarction; antigenic peptide.
 XX
 XX Unidentified.
 OS
 XX WO200056864-A2.
 PN
 XX 28-SEP-2000.
 PD
 XX 17-MAR-2000; 2000WO-GB001004.
 PF
 XX 19-MAR-1999; 99GB-00006245.
 PR
 XX (UYDU-) UNIV DUNDEE.
 PA
 PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 XX
 XX WPI; 2000-647155/62.
 DR
 XX
 XX Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide.
 XX
 XX Disclosure; Page 11; 103pp; English.
 PS
 XX This invention relates to a method for altering the substrate specificity
 CC of phosphoinositide-dependent protein kinase 1 (PKP1), by exposing it to
 CC an interacting polypeptide. Included in the invention are a preparation
 CC comprising PKP1 and an interacting polypeptide, PKP1 with altered
 CC specificity is useful for phosphorylating a residue corresponding to the
 CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
 CC -Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PKP1 is also used for phosphorylating
 CC protein kinase C related protein kinase 2 (PKR2). The compound identified
 CC by methods of the invention that are capable of altering the substrate
 CC specificity of PKP1 are useful for manufacturing a medicament for
 CC treating a patient who is in need of modulation of the insulin signalling
 CC pathway and/or PKP1, PKR2 or PKR2 signalling. A compound that is capable
 CC of reducing the activity (i.e. the PKP1 and/or the PKR2 activity) of PKP1
 CC may be useful in treating cancer. PKP1, e.g. via protein kinase B and/or
 CC SGK, may be capable of providing a survival signal that protects cells
 CC from apoptosis induced in a variety of ways. Reduction of the activity of
 CC PKP1 may promote apoptosis and may be useful in treating cancer.
 CC Conditions in which aiding apoptosis may be of benefit may also include
 CC resolution of inflammation. A compound capable of increasing the activity
 CC of PKP1 may be useful in treating diabetes or obesity, or may be useful
 CC in inhibiting apoptosis. Increased activity of PKP1 may lead to increased
 CC levels of leptin, which may lead to weight loss. The compounds may
 CC suppress apoptosis, which may aid cell survival during or following cell
 CC damaging processes and in treating disease in which apoptosis is
 CC involved. Examples of the diseases include, mechanical (including heart)
 CC tissue injury or ischaemic disease, for example stroke and myocardial
 CC infarction, or neural injury. The present sequence represents a region of
 CC protein kinase C related protein kinase 2 (PKR2) which interacts with
 CC PKP1
 CC
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 36; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDFDY 6
 |||||
 Db 14 FRDFDY 19

RESULT 12
 ID AAY94726
 AAY94726
 ID AAY94726 standard; peptide; 24 AA.

XX AAY94726;
 XX
 XX 29-JAN-2001 (first entry)
 XX
 XX Peptide capable of altering substrate specificity of PDK1.

XX Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
 KW protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KW mechanical tissue damage; ischaemic disease; stroke;
 KW myocardial infarction; antigenic peptide.
 XX
 XX Unidentified.
 OS
 XX WO200056864-A2.
 XX
 XX 28-SEP-2000.
 XX
 XX 17-MAR-2000; 2000WO-GB001004.
 XX
 XX 19-MAR-1999; 99GB-00006245.
 XX
 XX (UYDU-) UNIV DUNDEE.
 PA
 PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 XX
 XX WPI; 2000-647155/62.
 XX
 XX Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide.
 XX
 XX Disclosure; Page 9; 103pp; English.

XX This invention relates to a method for altering the substrate specificity
 CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
 CC an interacting polypeptide. Included in the invention are a preparation
 CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
 CC specificity is useful for phosphorylating a residue corresponding to the
 CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
 CC Ser-Phe/Tyr-ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
 CC protein kinase C related protein kinase 2 (PRK2). The compound identified
 CC by methods of the invention that are capable of altering the substrate
 CC specificity of PDK1 are useful for manufacturing a medicament for
 CC treating a patient who is in need of modulation of the insulin signalling
 CC pathway and/or PDK1, PKB2 or PKC2 signalling. A compound that is capable
 CC of reducing the activity (i.e. the PDK1 and/or the PKB2 activity) of PDK1
 CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
 CC SGK, may be capable of providing a survival signal that protects cells
 CC from apoptosis induced in a variety of ways. Reduction of the activity of
 CC PDK1 may promote apoptosis and may be useful in treating cancer.
 CC Conditions in which aiding apoptosis may be of benefit may also include
 CC resolution of inflammation. A compound capable of increasing the activity
 CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
 CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
 CC levels of leptin, which may lead to weight loss. The compounds may
 CC suppress apoptosis, which may aid cell survival during or following cell
 CC damaging processes, and in treating disease in which apoptosis is
 CC involved. Examples of the diseases include, mechanical (including heart)
 CC tissue injury or ischaemic disease, for example stroke and myocardial
 CC infarction, or neural injury. The present sequence represents a potential
 CC PDK1 substrate peptide. The peptide is capable of altering the substrate
 CC specificity of PDK1 in the method of the invention

XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 36; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDFDY 6
 |||||
 Db 14 FRDFDY 19

RESULT 13
 ID AAB99799
 AAB99799
 ID AAB99799 standard; peptide; 24 AA.

XX AAB99799;
 XX
 XX 20-SEP-2001 (first entry)
 XX
 XX Protein kinase derived interacting peptide #1.

XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;
 KW diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200144497-A2.
 XX
 XX 21-JUN-2001.
 XX
 XX 04-DEC-2000; 2000WO-GB004598.
 XX
 XX 02-DEC-1999; 99US-0168559P.
 XX
 XX (UYDU-) UNIV DUNDEE.
 PA
 PI Alessi D, Biondi R;
 XX
 XX WPI; 2001-390252/41.
 XX
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides.
 XX
 XX Disclosure; Page 25; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of a
 CC hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
 CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
 CC polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient in
 CC need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is in
 CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or composition
 CC is also useful for inhibiting the degree or rate of phosphorylation by
 CC the protein kinase. The interacting polypeptide or compound is useful in
 CC methods of stabilising a hydrophobic pocket-containing protein kinase,
 CC where the protein kinase is exposed to the compound or polypeptide.
 CC AAB99786 to AAB99847 represent amino acid sequences, and AAB44210 and
 CC AAB44211 represent oligonucleotide sequences, used in the exemplification
 CC of the present invention
 XX Sequence 24 AA;
 SQ

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
14 FRDPDY 19

Db

RESULT 14
AAB9794
ID AAB9794 standard; peptide; 24 AA.
AC AAB9794;
XX
XX
DT 20-SEP-2001 (first entry)
XX
DE 3-phosphoinositide-dependent protein kinase 1 binding peptide PIFide.
XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;
XX diabetes; inhibition; apoptosis; tissue injury; ischemic injury; stroke.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200144497-A2.
XX
XX 21-JUN-2001.
XX
XX 04-DEC-2000; 2000WO-GB004598.
XX
XX 02-DEC-1999; 99US-0168559P.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Alessei D, Biondi R;
PI
XX WPI; 2001-390252/41.
DR
XX
XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides.
XX
XX
XX Disclosure; Page 22; 180pp; English.
XX
XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of a
CC hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for
CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or
CC polynucleotides from the present invention are useful in medicine.
CC Particularly in the manufacture of a medicament for treating a patient in
CC need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is in
CC need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischemic injury, including stroke. The compound or composition
CC is also useful for inhibiting the degree or rate of phosphorylation by
CC the protein kinase. The interacting polypeptide or compound is useful in
CC methods of stabilising a hydrophobic pocket-containing protein kinase,
CC where the protein kinase is exposed to the compound or polypeptide.
CC AAB9786 to AAB9847 represent amino acid sequences, and AAB44210 and
CC AAB44211 represent oligonucleotide sequences, used in the exemplification
CC of the present invention
XX
XX
XX Sequence 24 AA;

Query Match 100.0%; Score 36; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
14 FRDPDY 19

Db

RESULT 15
ABR57451
ID ABR57451 standard; peptide; 24 AA.
XX
XX ABR57451;
AC
XX
XX 15-SEP-2003 (first entry)
XX
XX PKB activity modulating peptide #15.
DE
XX
XX Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
XX protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;
XX neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
XX structural analysis; cancer; diabetes; erectile dysfunction;
XX neurodegeneration.
XX
XX Synthetic.
OS
XX WO2003016516-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-GB003735.
XX
XX 14-AUG-2001; 2001GB-00019860.
XX
XX 01-MAY-2002; 2002GB-00009985.
XX
XX (NOVS) NOVARTIS FORSCHUNGSSIFTFUNG ZWEIGNIEDERL.
XX (CANC-) CANCER RES INST.
XX
XX Barford D, Yang J, Hemmings BA, Cron PD;
XX
XX WPI; 2003-268328/26.
DR
XX
XX New crystal of protein kinase B beta, useful for activating protein
PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
PT or a tetragonal space group.
XX
XX
XX Claim 32; Page 265; 284pp; English.
XX
XX The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising (1), where (1) comprises: (a) a tetragonal space
CC group P4₁-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
CC the specification. (1) has cytostatic, antidiabetic, vasotropic,
CC neurotropic and neuroprotective activities, and can be used in gene
CC therapy. The crystal of PKBbeta, and methods from the present invention,
CC are useful in activating protein kinases, particularly AGC kinases, for
CC identifying modulators of protein kinase activity, and for structural
CC analysis of other protein kinases. The crystal may also be used in
CC manufacturing a medicament for treating cancers, diabetes, erectile
CC dysfunction or neurodegeneration. The present sequence represents a
CC peptide which can be used in a method from the present invention to
CC modulate PKB activity
XX
XX
XX Sequence 24 AA;

Query Match 100.0%; Score 36; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
|||
Db 14 FRDPDY 19

Search completed: June 14, 2006, 02:09:01
Job time : 157.5 secs

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:58 ; Search time 218 Seconds
(Without alignments)
25.459 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fpgfsy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	27	2	06PWW2_CANFA
2	35	100.0	36	2	09N1C5_BOVIN
3	35	100.0	37	2	09N1C6_SHEEP
4	35	100.0	66	2	06PWW1_CANFA
5	35	100.0	198	2	08C6X4_MOUSE
6	35	100.0	201	2	09BV07_HUMAN
7	35	100.0	246	2	09PUJ3_CHICK
8	35	100.0	256	2	09N582_CAEEL
9	35	100.0	302	2	04TBD9_TETNG
10	35	100.0	353	2	08CE74_MOUSE
11	35	100.0	419	2	0519W5_CANFA
12	35	100.0	472	2	04SLA7_TETNG
13	35	100.0	478	2	0802Y3_BRARE
14	35	100.0	479	1	AKT3_HUMAN
15	35	100.0	479	1	AKT3_MOUSE
16	35	100.0	479	2	05VTI1_HUMAN
17	35	100.0	479	2	06NXX0_MOUSE
18	35	100.0	480	1	AKT1_BOVIN
19	35	100.0	480	1	AKT1_HUMAN
20	35	100.0	480	1	AKT1_MOUSE
21	35	100.0	480	1	AKT1_RAT
22	35	100.0	480	2	05ER56_BOVIN
23	35	100.0	480	2	06GSA6_MOUSE
24	35	100.0	480	2	057513_CHICK
25	35	100.0	481	1	AKT1_XENLA
26	35	100.0	481	1	AKT2_HUMAN
27	35	100.0	481	1	AKT2_MOUSE
28	35	100.0	481	1	AKT2_RAT
29	35	100.0	481	2	03HSE5_RAT
30	35	100.0	481	2	03TY95_MOUSE
31	35	100.0	485	1	AKT2B_XENLA

32	35	100.0	486	1	AKT2A_XENLA	07zx15 xenopus lae
33	35	100.0	501	1	AKT MLVAT	p31748 akt8 murine
34	35	100.0	523	2	04T057_TETNG	04t057 tetradon n
35	35	100.0	611	1	AKT1_DROME	08ind9 drosophila
36	32	91.4	96	2	04MNG3_BACCE	04mng3 bacillus ce
37	32	91.4	96	2	0637M0_BACCE	0637m0 bacillus ce
38	32	91.4	96	2	06HFJ2_BACCH	06hfj2 bacillus th
39	32	91.4	96	2	081Y91_BACAN	081y91 bacillus an
40	32	91.4	96	2	0733N3_BACCI	0733n3 bacillus ce
41	32	91.4	101	2	03EDM1_BACTI	03edm1 bacillus th
42	32	91.4	101	2	0812Z5_NITOC	0812z5 bacillus ce
43	32	91.4	102	2	03JAI5_NITOC	03jai5 nitrosococ
44	32	91.4	175	2	036GM8_9GAMM	036gm8 shewanella
45	32	91.4	254	2	03HG86_TRIER	03hg86 trichodesmi

ALIGNMENTS

RESULT 1
06PWW2_CANFA PRELIMINARY; PRT; 27 AA.
AC 06PWW2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
OS Protein Kinase B gamma-like protein (Fragment).
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Muria Escobar H., Meyer J., Winkler S., Schelling C., Dolf G.,
RA Nolte I., Bullerdiek J.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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CC EMBL: AY575065; AAS89304.1; -; Genomic DNA.
DR Ensembl: ENSCARG0000015806; Canis familiaris.
DR GO: GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON TER 1
SQ SEQUENCE 27 AA; 3145 MW; E65A150C3808A39A CRC64;

Query Match 100.0%; Score 35; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPGFSY 6
Db 16 FPGFSY 21

RESULT 2
09N1C5_BOVIN PRELIMINARY; PRT; 36 AA.
AC 09N1C5;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Protein kinase B (Fragment).
GN Name=AKT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RX MEDLINE=20458865; PubMed=11003702; DOI=10.1007/s003350010150;
RA Fahrnkung S.C., Freking B.A., Rexroad C.E. III, Leymaster K.A.,
RA Kappes S.M., Smith T.P.L.;
RT "Comparative mapping of the ovine clpg locus.";
RL Mamm. Genome 11:871-876(2000).
CC -----
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CC -----
DR EMBL, AF207874; AAF67084.1; -, Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER
SQ SEQUENCE 36 AA; 4055 MW; EFC17D6728155130 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 25 PPOFSY 30

RESULT 3
ID O9N1C6_SHEEP PRELIMINARY; PRT; 37 AA.
AC O9N1C6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Protein kinase B (Fragment).
GN Name=AKT;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fahrnkung S.C., Freking B.A., Rexroad C.E. III, Leymaster K.A.,
RA Kappes S.M., Smith T.P.L.;
RT "Comparative mapping of the ovine clpg locus.";
RL Mamm. Genome 0:0-0(2000).
CC -----
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CC -----
DR EMBL, AF207873; AAF67083.1; -, Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER
SQ SEQUENCE 37 AA; 4115 MW; 9AA56E9B5C894882 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 26 PPOFSY 31

RESULT 4
ID O6PVM1_CANFA PRELIMINARY; PRT; 66 AA.
AC O6PVM1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Protein kinase B gamma-like protein (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Murua Escobar H., Borrmann L., Nimzyk R., Nolte I., Bullerdiek J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL, AY575066; AAS89305.1; -, mRNA.
DR Ensembl, ENSCAFG0000015806; Canis familiaris.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro, IPR000961; Pkinase_C.
DR Pfam, PF00433; Pkinase_C; 1.
DR SMART, SM00133; S_TK_X; 1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 66 AA; 7752 MW; 0A08B63B19BE68C7 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 55 PPOFSY 60

RESULT 5
ID Q8C6X4_MOUSE PRELIMINARY; PRT; 198 AA.
AC Q8C6X4;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE 15 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:D930002M15 product:thymoma viral proto-oncogene 3, full insert
DE sequence. (Fragment).
GN Name=Akt3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christofideis A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Heminger P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humnick L., Iacono M., Iakeo K., Iwama A., Ishikawa T.,

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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Livovich L., Liu J.,
 RA Luna S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motegut-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Schobach C., Sekiguchi K., Sempke C.A., Seno S., Seesa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tamajo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimiyu N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi H., Bono H., Kondo S.,
 RA Nkaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brack D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazar K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guelinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haeizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bara G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker G., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kusunagi T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
 RA Yamamoto R., Matsunoto H., Sakaeguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hamaguchi T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK052953; BAC35219.1; -; mRNA.
 DR HSSP: P31751; IMRY.
 DR SRR: O8C6X4; 1-178.
 DR Ensembl: ENSMUSG00000019699; Mus musculus.
 DR MGI: MGI.1345147; Akt3.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000961; Kinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Kinase_I.
 DR Pfam: PF00433; Kinase_C; 1.

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
FT NON TER 1
SQ SEQUENCE 198 AA; 22644 MW; 242F9CDD03C7ABE9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 198;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 187 PPOFSY 192

RESULT 6
Q9BV07_HUMAN PRELIMINARY; PRT; 201 AA.
AC Q9BV07;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC001737; AAH01737.1; -; mRNA.
DR HSSP; P31751; IMRY.
DR SMR; Q9BV07; 1-183.
DR Ensembl; ENSG00000142208; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 201 AA; 23017 MW; C3441BC52259AB3D CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 201;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 190 PPOFSY 195

RESULT 7
Q9PUJ3_CHICK PRELIMINARY; PRT; 246 AA.
AC Q9PUJ3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Protein serine/threonine kinase (Fragment).

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GN Name=AKT2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA MEDLINE=21218646; PubMed=11319165;
RA Johnson A.L., Bridgham J.T., Swenson J.A.;
RT "Activation of the Akt/protein kinase B signaling pathway is
RT associated with granulosa cell survival.";
RL Biol. Reprod. 64:1566-1574(2001).

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DR EMBL; AF181260; AAD54413.1; -; mRNA.
DR HSSP; P31751; IMRY.
DR SMR; Q9PUJ3; 1-228.
DR Ensembl; ENSGALG0000011620; Gallus gallus.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 246 AA; 28570 MW; CCAFAA3BBE1DBED CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 246;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
Db 235 PPOFSY 240

RESULT 8
Q9NS82_CAEEL PRELIMINARY; PRT; 256 AA.
AC Q9NS82;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 2.
DT 07-FEB-2006, entry version 30.
DE Hypothetical protein.
GN CRNames=Y119CIA.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- INTERACTION:

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CC 01670:eva-1; NbExp=1; IntAct=EBI-315836, EBI-311862;
CC 020485:466g1.1; NbExp=1; IntAct=EBI-315836, EBI-3122655;
CC 022534:sei-16; NbExp=1; IntAct=EBI-315836, EBI-327662;
CC 097238:sei-4; NbExp=1; IntAct=EBI-315836, EBI-329192;
CC 019969:ima-3; NbExp=1; IntAct=EBI-315836, EBI-317340;
CC 090978:jit-1; NbExp=1; IntAct=EBI-315836, EBI-318513;
CC 045521:thr-11; NbExp=1; IntAct=EBI-315836, EBI-313336;
CC 009485:py-1; NbExp=1; IntAct=EBI-315836, EBI-315739;
CC 045784:caf-9; NbExp=1; IntAct=EBI-315836, EBI-327711;
CC 017359:vab-3; NbExp=1; IntAct=EBI-315836, EBI-319610;
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CC -----
DR EMBL: AC006709; AAF60432.2; -; Genomic_DNA.
DR IntAct: Q9N582; -
DR Ensembl: Y119C1A.1; Caenorhabditis elegans.
DR Wormbase: WBGene0002466; Y119C1A.1.
DR GO: GO:0005515; F:protein binding; IPI.
DR InterPro: IPR002052; N6_Mcase.
DR InterPro: IPR001876; ZnF_RanBP2.
DR PROSITE: PS00092; N6_MTase; UNKNOWN_1.
DR PROSITE: PS01358; ZF_RANBP2_1; 1.
DR PROSITE: PS50199; ZF_RANBP2_2; 1.
SQ Complete proteome; Hypothetical protein.
SQ SEQUENCE 256 AA; 28520 MM; DD279034AAAF77382 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PROFSY 6
Db 23 PROFSY 28

RESULT 9
QATBD9_TETNG PRELIMINARY; PRT; 302 AA.
ID QATBD9_TETNG
AC QATBD9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Chromosome undetermined SCAF7139, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0003798001;
OS Tetradon nigrovittidis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ublin C., Castellani V., Katinika M., Vachere B.,
RA Biemond C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
RA Cnuand C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Keills M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollis H.;
RT "Genome duplication in the teleost fish Tetradon nigrovittidis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

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RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
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CC -----
DR EMBL: CAAE01007139; CAF89793.1; -; Genomic_DNA.
DR SMR: QATBD9; 40-235.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00106; PROTEIN_KINASE_ST; 1.
DR KW ATP-binding; Kinase; Nucleotide-binding;
FM Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 302
FT SEQUENCE 302 AA; 34209 MM; 32D4564122D5855F CRC64;

Query Match 100.0%; Score 35; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PROFSY 6
Db 291 PROFSY 296

RESULT 10
Q8CE74_MOUSE PRELIMINARY; PRT; 353 AA.
ID Q8CE74_MOUSE
AC Q8CE74;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 10 days neonate skin cDNA, RIKEN full-length enriched library,
DE clone:473245F20 product:chymoma viral proto-oncogene 2, full insert
DE sequence. (Fragment).
GN Name=Akt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MBLINB=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lennarz S.E., Baldov S., Forrest A.R., Zavelan M.,
 Davis M.J., Wilmshurst L.G., Adkins V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banasi M., Baxter K., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Habbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Motenaghi-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada K., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,
 RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nishimura N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tashiro M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=2254663; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishio T., Ohsato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochua C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nomura K., Okita T., Pavan W.J., Perte G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Tesdale R.D., Tomita M.,
 RA Verardo R., Wagner T., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavelan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirokawa-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okida T., Furuno M., Kono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-Format
 sequencing pipeline with 384 multichannel sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takada Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBS databases.
 CC -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: AK028671; BAC26162.1; -; mRNA.
DR HSSP: P31751; 1MR.
DR Ensembl: ENSMUSG00000004056; Mus musculus.
DR MGI: MGI:104874; Akt2.
DR GO: GO:0030027; C:lamellipodium; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0046328; P:regulation of JNK cascade; IDA.
DR InterPro: IPR000961; Kinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Ehr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00433; Kinase C; 1.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TKc; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 353 AA; 40766 MW; 325D23F43975FFD7 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 342 FPOFSY 347

RESULT 11
ID 0519W5_CANFA PRELIMINARY; PRT; 419 AA.
AC 0519W5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protein kinase B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu P., Colitz C.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: AY833721; AAW52726.1; -; mRNA.
DR SMR: 0519W5; 1-49.
DR Ensembl: ENSMUSG00000005388; Canis familiaris.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH_type.
DR InterPro: IPR000961; Kinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Kinase; 1.

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DR Pfam: PF00433; Kinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00133; S_TKc; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KM Kinase.
SQ SEQUENCE 419 AA; 48357 MW; 14CE64B62F7043C CRC64;

Query Match 100.0%; Score 35; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
DB 408 FPOFSY 413

RESULT 12
ID 04SLA7_TETNG PRELIMINARY; PRT; 472 AA.
AC 04SLA7;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Chromosome 7 SCFA14557, whole genome shotgun sequence.
GN ORFNames=GSTENG00016324001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Kallinka M., Vachere B.,
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Couranceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.-J., McEwan P., Bosak S.,
RA Kellis M., Volt J.-N., Guigo R., Zody M.C., Westrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weisenbach J., Roest Crollius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -! SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -! SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -! SIMILARITY: Contains 1 PH domain.
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CC -----

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DR EMBL: CAE01014557; CAF98575.1; -; Genomic_DNA.
 DR SMR; Q4SLA7; 1-103.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR Prodom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 472 AA; 54836 MW; F9448E88D55273B CRC64;

Query Match 100.0%; Score 35; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
 Db 461 PPOFSY 466

RESULT 13
 ID Q802Y3_BRAE PRELIMINARY; PRT; 478 AA.
 AC Q802Y3;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE V-akt murine thymoma viral oncogene homolog 2, like.
 GN Name=akt21;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Manisina K., Farrow A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Mada A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.,
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 1 PH domain.
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 CC -----
 DR EMBL: BC046892; AAH46892.1; -; mRNA.
 DR HSSP; P31751; IMRV.
 DR SMR; Q802Y3; 1-111.
 DR Ensembl; ENSDARG00000026797; Danio rerio.
 DR ZFIN; ZDB-GENE-040121-5; akt21.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR Prodom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 478 AA; 55452 MW; F7B5AB68428A7A6A CRC64;

Query Match 100.0%; Score 35; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPOFSY 6
 Db 467 PPOFSY 472

RESULT 14
 ID AKT3_HUMAN STANDARD; PRT; 479 AA.
 AC Q9Y243; Q960V3; Q9UPP5;
 DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999, sequence version 1.
 DT 07-MAR-2006, entry version 59.
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 GN (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STR-2).
 GN Name=AKT3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND MUTAGENESIS.
 RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;

RA Brodbeck D., Cron P., Hemmings B.A.;
 RT "A human protein kinase B gamma with regulatory phosphorylation sites
 in the activation loop and in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 274:9133-9136(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=99255329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;
 RA Nakatani K., Sakae H., Thompson D.A., Weigelt R.J., Roth R.A.;
 RT "Identification of a human Akt3 (protein kinase B gamma) which
 contains the regulatory serine phosphorylation site.";
 RL Biochem. Biophys. Res. Commun. 257:906-910(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=99421751; PubMed=10491192;
 RA Masuie S., Haefliger B., Weeslink J.-J., Hoefnagel E., Mortier E.,
 Verhaesselt P., Tuytelaars A., Gordon R., Richardson A.;
 RT "Molecular cloning, expression and characterization of the human
 serine/threonine kinase Akt-3.";
 RL Eur. J. Biochem. 265:353-360(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RA Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;
 RT "Cloning of a novel human cDNA, STR-2, which encodes a rat serine-
 threonine protein kinase (STR) homolog.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
 RC TISSUE=Testis;
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wemm S., Weill B., Wellenreuther R., Gassenhuber J., Glaesl S.,
 Ansoorge W., Boecker M., Bioecker H., Bauersachs S., Blum H.,
 Lauber J., Duesterhoeft A., Beyer A., Koehner K., Strack N.,
 Mewes H.-W., Oetemaelder B., Obermaier B., Tampe J., Heubner D.,
 Wandt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND MUTAGENESIS OF
 THR-305 AND THR-447.
 RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
 RA Brodbeck D., Hill M.M., Hemmings B.A.;
 RT "Two splice variants of PKB gamma have different regulatory capacity
 depending on the presence or absence of the regulatory phosphorylation
 site Ser-472 in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 276:29550-29558(2001).
 CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 role in regulating cell survival. Capable of phosphorylating
 several known proteins. Truncated isoform 2/PKB gamma 1 without
 the second serine phosphorylation site could still be stimulated
 but to a lesser extent.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- INTERACTION:
 CC O16543: CDC37; NBEXP=1; Intact=EBI-296115, EBI-295634;
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 cell stimulation leading to its translocation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=PKB gamma;
 CC IsoId=O9Y243.1; Sequence=Displayed;
 CC Name=2; Synonyms=PKB gamma 1;
 CC IsoId=O9Y243.2; Sequence=VSP_004947;
 CC -1- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in
 brain, lung and kidney, but weakly in heart, testis and liver. In
 fetal tissues, it is highly expressed in heart, liver and brain
 and not at all in kidney.
 CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 kinase alpha (PI(3)K) results in its targeting to the plasma
 membrane.
 CC -1- PTM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both serines and threonines is required for
 full activity.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 subfamily.
 CC -1- SIMILARITY: Contains 1 PH domain.
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 CC -----
 DR EMBL: AF124141; AAD29089.1; -; mRNA.
 DR EMBL: AF135794; AAD24196.1; -; mRNA.
 DR EMBL: AF085234; AAL40392.1; -; mRNA.
 DR EMBL: AF045709; CAB53537.1; -; mRNA.
 DR EMBL: AL117525; CAB55977.1; ALT_TERM; mRNA.
 DR EMBL: AY005799; AAF91073.1; -; mRNA.
 DR PIR: A59380; A59380.
 DR HSP: P31751; IGZK.
 DR SMR: O9Y243; 1-115.
 DR IntAct: O9Y243; -.
 DR Ensembl: ENSG00000117020; Homo sapiens.
 DR HGNC: HGNC:393; AKT3.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0004672; F:protein kinase activity; TAS.
 DR GO: GO:000468; F:protein amino acid phosphorylation; TAS.
 DR GO: GO:007165; P:signal transduction; TAS.
 DR InterPro: IPR01849; PH.
 DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Kinase C.
 DR InterPro: IPR008271; Ser_Thr_kin_AS.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00433; Kinase C; 1.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PSS0003; PH DOMAIN; 1.
 DR PROSITE: PSS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PSS00108; PROTEIN_KINASE_ST; 1.
 DR KMW: Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
 RT Phosphorylation; Serine/threonine-protein kinase; Transferase.
 RT CHAIN 1 479
 FT
 FT DOMAIN 5 107
 FT
 FT DOMAIN 148 405
 FT NP_BIND 154 162
 FT ACT_SITE 271 271
 FT BINDING 177 177
 FT MOD_RES 305 305
 FT MOD_RES 472 472
 FT VARSPPLIC 452 479
 FT
 FT MUTAGEN 305 305
 FT
 FT MUTAGEN 305 305
 FT
 FT MUTAGEN 447 447
 FT MUTAGEN 447 447
 FT MUTAGEN 472 472
 FT
 FT MUTAGEN 472 472
 FT
 FT SEQUENCE 479 AA; 5575 MW; F08BDB502E78B CRC64;
 SQ
 Query Match 100.0%; Score 35; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 75;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPOFSY 6
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 Db 468 PPOFSY 473

RESULT 15
 AKT3 MOUSE STANDARD; PRT; 479 AA.
 AC Q9WUA6;
 DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1999, sequence version 1.
 DT 07-MAR-2006, entry version 50.
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 GN (Protein kinase Akt-3) (protein kinase B, gamma) (PKB gamma).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE:99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
 RA Brobeck D., Cron P., Hemmings B.A.;
 RT "A human protein kinase B gamma with regulatory phosphorylation sites
 in the activation loop and in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 274:9133-9136(1999).
 CC [2]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RP TISSUE=Brain;
 RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
 RA Brobeck D., Hill M.M., Hemmings B.A.;
 RT "Two splice variants of PKB gamma have different regulatory capacity
 depending on the presence or absence of the regulatory phosphorylation
 site Ser-472 in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 276:29550-29558(2001).
 CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 role in regulating cell survival. Capable of phosphorylating
 several known proteins. Truncated isoform 2/PKB gamma 1 without
 the second serine phosphorylation site could still be stimulated
 but to a lesser extent (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 cell stimulation leading to its translocation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=PKB gamma;
 CC IsoId=Q9WUA6-1; Sequence=Displayed;
 CC Name=2; Synonyms=PKB gamma 1;
 CC IsoId=Q9WUA6-2; Sequence=VSP_004948;
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in prostate, testis,
 uterus and mammary gland and isoform 2 is expressed in prostate,
 testis and mammary gland.
 CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 kinase alpha (PI(3)K) results in its targeting to the plasma
 membrane.
 CC -1- PTM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both sites is required for full activity.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 subfamily.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -----
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 CC -----
 CC EMBL: AF124142; AAD29090.1; -; mRNA.
 CC HSSP: P31751; 1GZK.
 CC SMR: Q9WUA6; 1-115.
 CC DR Ensembl: ENSMUSG00000019699; Mus musculus.
 CC MGI: MGI:1345147; Akt3.
 CC InterPro: IPR001849; PH.

DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Kinase C.
 DR InterPro: IPR000719; Prot Kinase.
 DR InterPro: IPR008271; Ser_thr_kin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF00433; Kinase C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00220; S_TKC; 1.
 DR PROSITE: PS50003; PH DOMAIN; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
 DR Alternative splicing: ATP-binding; Kinase; Nucleotide-binding;
 KW phosphorylation; Serine/threonine-protein kinase; Transferase.
 FT CHAIN 1 479 RAC-gamma serine/threonine-protein kinase.
 FT /FTId=PRO_0000085612.
 FT
 FT DOMAIN 5 107 PH.
 FT 148 405 Protein kinase.
 FT NP_BIND 154 162 ATP (By similarity).
 FT ACT_SITE 271 271 Proton acceptor (By similarity).
 FT BINDING 177 177 ATP (By similarity).
 FT MOD_RES 305 305 Phosphothreonine (By similarity).
 FT MOD_RES 472 472 Phosphoserine (By similarity).
 FT VARSP_LIC 452 479 YDDGMDGMDNRRRPHPPQFSYSASGR -> CQOSDCGML
 FT GNWKKNDNRK (in isoform 2).
 FT /FTId=VSP_004948.
 SQ SEQUENCE 479 AA; 55714 MW; F08ACDF5743B8FB CRC64;

Query Match 100.0%; Score 35; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPOFSY 6
 |||||
 Db 468 PPOFSY 473

Search completed: June 14, 2006, 02:16:28
 Job time : 220 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:03:58 ; Search time 218 Seconds
(without alignments).
25.459 Million cell updates/sec

Title: 09937009-A
Perfect score: 36
Sequence: 1 frdfdy 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	60	2	06PSW9 HUMAN
2	36	100.0	234	2	066WK2 FELIS silve
3	36	100.0	389	2	04CT57 TRYICR
4	36	100.0	389	2	0580R7 TRYANOSOMA
5	36	100.0	392	2	042262 XENLA
6	36	100.0	539	2	03GY02 NACTO
7	36	100.0	585	2	097KY8 CLOAB
8	36	100.0	786	1	TIR1 HUMAN
9	36	100.0	786	2	032MK3 HUMAN
10	36	100.0	786	2	032MK4 HUMAN
11	36	100.0	786	2	05FMG5 HUMAN
12	36	100.0	786	2	06F1G4 HUMAN
13	36	100.0	796	2	04LDR7 PIG
14	36	100.0	796	2	059H19 PIG
15	36	100.0	966	2	04RZ53 TETNG
16	36	100.0	984	1	PKN2 HUMAN
17	33	91.7	114	2	05A758 CANAL
18	33	91.7	142	2	05A7D3 CANAL
19	33	91.7	168	2	094044 CANAL
20	33	91.7	210	2	025450 HELPY
21	33	91.7	235	2	092L68 HELPY
22	33	91.7	254	2	09XY00 RHAYDO
23	33	91.7	261	2	07NS51 PHOLA
24	33	91.7	348	2	08MU12 PHILA
25	33	91.7	352	1	LARK DROME
26	33	91.7	434	1	KESI YEAST
27	33	91.7	434	1	060511 YEAST
28	33	91.7	437	2	02V2Y4 ANATH
29	33	91.7	437	2	06FJ22 CANGA
30	33	91.7	464	1	MOC3 ARATH
31	33	91.7	511	2	08YV02 ANASP

32	33	91.7	529	2	09FK32 ARATH	09FK32 arabidopsis
33	33	91.7	598	2	05AID5 CANAL	05AID5 candida alb
34	33	91.7	611	2	02QW73 TORSA	02QW73 cryza sativ
35	33	91.7	611	2	05MAU8 ARATH	05MAU8 arabidopsis
36	33	91.7	613	2	09LXK4 ARATH	09LXK4 arabidopsis
37	33	91.7	664	1	04FGB2 CLOPE	04FGB2 clostridium
38	33	91.7	691	2	04FPE8 PELUB	04FPE8 pelagibacte
39	33	91.7	724	2	02UNN2 ASPOR	02UNN2 aspergillus
40	33	91.7	870	2	054Q71 DICDI	054Q71 dictyosteli
41	33	91.7	881	2	081L19 PLARF	081L19 plasmodium
42	33	91.7	881	2	09BKN8 PLARA	09BKN8 plasmodium
43	33	91.7	895	1	FL0D MIMIV	05GK3 mimivirus
44	33	91.7	993	1	NISB LACTA	P20103 lactococcus
45	33	91.7	993	2	048673 GLACT	048673 lactococcus

ALIGNMENTS

RESULT 1
ID 06PSW9_HUMAN PRELIMINARY; PRT; 60 AA.
AC 06PSW9;
DT 05-JUL-2004, integrated into UniprotKB/TREMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE PKN2 protein.
GN Name=PKN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stedington M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Toehiyki S., Carninci P., Prange C.C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalana D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BC062620; AA62620.1; -; mRNA.
CC Ensembl: ENSG00000065243; Homo sapiens.
CC GO: GO:0005524; F:ATP binding; IEA.
CC GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
CC GO: GO:0006468; P:Protein amino acid phosphorylation; IEA.
CC InterPro: IPR000961; Kinase_C.
CC Pfam: PF00433; Kinase_C; 1.

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DR SMART; SM00133; S.TK.X; 1.
SQ SEQUENCE 60 AA; 7149 MW; 6CB26D2FB270F7D7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
   |||||
Db 50 FRDPDY 55

RESULT 2
066WK2_FELCA PRELIMINARY; PRT; 234 AA.
AC 066WK2;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE Toll-like receptor 1 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15963821; DOI=10.1016/j.yetimm.2005.02.022;
RA Ignacio G., Nordone S., Howard K.E., Dean G.A.;
RT "Toll-like receptor expression in feline lymphoid tissues.";
RL Vet. Immunol. Immunopathol. 106:229-237(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Ignacio G.A., Dean G.A.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY00368; AUI12171.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 27070 MW; D0D466B0DB601BCE CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 234;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
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Db 105 FRDPDY 110

RESULT 3
04CT57_TRYCR PRELIMINARY; PRT; 389 AA.
AC 04CT57;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Trypophanyl-tRNA synthetase, putative (EC 6.1.1.2).
GN ORFNames=TC00.1047053510647.30;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Schizotrypanum
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;

```

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RA El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA Haas B., Anupama A., Arner E., Aslund U., Atcioppe P., Bontempi E.,
RA Bringard F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA Englund P.T., Fazellina G., Feldblum T., Ferreira M., Frasch A.C.,
RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA Nelson S., Ochaya S., Osogawa K., Pal G., Parsons M., Pentony M.,
RA Petersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA Fraser C.M., Stuart K.D., Anderson B.,
RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RT Disease.";
RL Science 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Bader J.,
RA Bringard F., Cadag E., Carlson J.M., Cerqueira G.C., Greasy T.,
RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA Salzberg S.L., Shallow J., Silva J.C., Sundaram J., Westenberger S.,
RA White O., Melville S.E., Donelson J.E., Anderson B., Stuart K.D.,
RA Hall N.;
RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL Science 0:0-0(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL Brener;
RA El-Sayed N., Bartholomeu D., Haas B.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAHK01001949; EAN83677.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp_tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA_tRNA_ligase_1; UNKNOWN_1.
KM Aminoacyl-tRNA synthetase, ligase.
SQ SEQUENCE 389 AA; 44316 MW; A1F94B797CC42FD8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 389;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
   |||||
Db 152 FRDPDY 157

RESULT 4
0580R7_9TRYP PRELIMINARY; PRT; 389 AA.
AC 0580R7;

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DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DE 07-FEB-2006, entry version 3.
 DE Trypophanyl-tRNA synthetase, putative (EC 6.1.1.2).
 GN ORFNames=TB927.3.5580;
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUtact10.1;
 RA Ghedin E., Blandin G., Bartholomew D., Caler E., Haas B., Hannick L.,
 RA Shallem J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalek H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Manles D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUtact10.1;
 RA El-Sayed N.M., Khalek H., Adams M.D.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUtact10.1;
 RA Haas B., Blandin G., El-Sayed N.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AC093543; AAX81067.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016874; F:Ligase activity; IEA.
 DR GO: GO:0004830; F:Cryptophan-tRNA ligase activity; IEA.
 DR GO: GO:0006436; F:Cryptophanyl-tRNA aminoacylation; IEA.
 DR InterPro: IPR002305; tRNA-synt_1b.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR InterPro: IPR002306; TRP-tRNA-synt_1b.
 DR Pfam: PF00579; tRNA-synt_1b; 1.
 DR PRINTS: PRO1039; TRNASYNTHTRP.
 DR TIGRFAMs: TIGR00233; trps; 1.
 DR PROSITE: PS00178; AA tRNA ligase; 1.
 DR Anticodon-tRNA synthetase; ligase
 SQ SEQUENCE 389 AA; 44246 MW; F887BF8A066CA27 CRC64;
 Query Match 100.0%; Score 36; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRDPDY 6
 DB 152 FRDPDY 157
 RESULT 5
 ID 042262_XENLA PRELIMINARY; PRT; 392 AA.
 AC 042262;
 DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
 DT 01-JAN-1998, sequence version 1.
 DE 07-FEB-2006, entry version 28.
 DE Protein kinase C-related kinase 2 (Fragment).
 GN Name=PRK2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98037762; PubMed=9368003; DOI=10.1074/jbc.272.47.29449;
 RA Cryns V.L., Byun Y., Rana A., Mellor H., Lustig K.D., Ghanem L.,

RA Parker P.J., Kirschner M.W., Yuan J.;
 RT "Specific proteolysis of the kinase protein kinase C-related kinase 2
 RT by caspase-3 during apoptosis. Identification by a novel, small pool
 RT expression cloning strategy.";
 RL J. Biol. Chem. 272:29449-29453 (1997).
 CC 1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -----
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 CC -----
 DR EMBL: AF027183; AAC13357.1; -; mRNA.
 DR HSSP: P31751; IMRY.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:Protein kinase activity; IEA.
 DR GO: GO:0006468; P:Protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000961; Kinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00433; Kinase_C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 392 AA; 44960 MW; 76891B23ABC3C87 CRC64;
 Query Match 100.0%; Score 36; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRDPDY 6
 DB 382 FRDPDY 387
 RESULT 6
 ID 03GY02_9ACTO PRELIMINARY; PRT; 539 AA.
 AC 03GY02;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DE 07-FEB-2006, entry version 4.
 DE AMP-dependent synthetase and ligase.
 GN ORFNames=NocADRAFT_1748;
 OS Nocardioides sp. JS614.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Protonibacteriaceae; Nocardioidaceae; Nocardioides.
 NCBI_TaxID=196162;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JS614;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Nocardioides sp.
 RT JS614.";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JS614;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Nocardioides sp. JS614.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.

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CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
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CC -----
DR EMBL: AAIJ01000046; EAO06609.1; -; Genomic_DNA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
KW ligase.
SQ SEQUENCE 539 AA; 59725 MW; B6976197A620CFB CRC64;

Query Match 100.0%; Score 36; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 131 FRDPDY 136

RESULT 7
097KY8_CLOAB PRELIMINARY; PRT; 585 AA.
AC 097KY8;
DT 01-OCT-2001, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE ATP-dependent RNA helicase, superfamily II.
GN OrderedLocNames=CAC0778;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.V., Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RT J. Bacteriol. 183:4823-4838(2001).
CC -----
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CC -----
DR EMBL: AE007593; AAK78754.1; -; Genomic_DNA.
DR PIR: G96995; G96995.
DR BioCyc: CAC1488:CAC0778-MONOMER; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:000166; F:nucleotide binding; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00271; Helicase_G_1.
DR SMART: SMO0490; HELIC_G_1.
KW Complete proteome; Helicase.
SQ SEQUENCE 585 AA; 68643 MW; 849DFD42485D53 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 585;

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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 54 FRDPDY 59

RESULT 8
TLR1_HUMAN
ID TLR1_HUMAN STANDARD; PRT; 786 AA.
AC Q15399; O15452; Q9UG90;
DT 31-JAN-2002, integrated into UniProtKB/Swiss-Prot.
DT 31-JAN-2002, sequence version 2.
DT 07-MAR-2006, entry version 57.
DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like
DE protein) (TIR) (CD281 antigen).
GN Name=TLR1; Synonyms=K1AA0012;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Erythrocytopenia;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RA "A family of human receptors structurally related to Drosophila
RT Toll.",
RT Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026; DOI=10.1093/dnares/1.1.27;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi T.,
RA Sato S., Nagase T., Seki N., Ishikawa K., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RT DNA Res. 1:27-35(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassel S.,
RA Ansorge W., Boecker M., Bloeker H., Bautesachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Oettmayer B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RA "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RT Genome Res. 11:422-435(2001).
RN [4]
RP PROTEIN SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction, based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RA Xu Y., Tao X., Shen B., Horng T., Medhiov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domains.";
RL Nature 408:111-115(2000).
CC -!- FUNCTION: Participates in the innate immune response to microbial
CC agents. Cooperates with TLR2 and modulates the response to
CC microbial constituents. Acts via MYD88 and TRAF6, leading to NF-
CC kappa-B activation, cytokine secretion and the inflammatory
CC response (by similarity).

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CC -1- SUBUNIT: Binds TLR2 via their respective extracellular domains.
CC Binds MyD88 via their respective TIR domains (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (by similarity).
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,
CC peripheral blood leukocytes, thymus and small intestine.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 8 LRR (leucine-rich) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
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DR EMBL: U88540; AAC34137.1; -; mRNA.
DR EMBL: D13637; BAA02801.2; ALT_INTT; mRNA.
DR EMBL: AL050262; CAB3364.1; -; mRNA.
DR PIR: J08664; T08664.
DR PDB: 1FYV; X-ray; A=625-785.
DR Ensembl: ENSG00000174125; Homo sapiens.
DR H-invDB: HIX004160; -.
DR HGNC: HGNC:11847; TLR1.
DR MIM: 601194; gene.
DR GO: GO:0005887; C:Integral to plasma membrane; TAS.
DR GO: GO:0045335; C:phagocytic vesicle; ISS.
DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0004888; F:transmembrane receptor activity; NAS.
DR GO: GO:0042487; F:triacylated lipoprotein binding; ISS.
DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO: GO:0042495; P:detection of triacylated bacterial lipoprotein; ISS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0042116; P:macrophage activation; NAS.
DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR004075; IL1_rcpt_1.
DR InterPro: IPR001611; LRR_C.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_CYP.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PR01537; LEU1KXN1RF.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR 3D-structure: Direct protein sequencing; Glycoprotein;
KM Immune response; Inflammatory response; Innate immunity;
KM Leucine-rich repeat; Membrane; Polymorphism; Receptor; Repeat; Signal;
KM Transmembrane.
FT SIGNAL 25 24
FT CHAIN 1 786
FT TOPO_DOM 25 580 Toll-like receptor 1.
FT TRANSMEM 581 601 /FtId=PRO_0000034705.
FT TOPO_DOM 602 786 Extracellular (Potential).
FT REPEAT 68 786 Potential
FT REPEAT 91 113 Cytoplasmic (Potential).
FT REPEAT 114 137 LRR 1.
FT REPEAT 139 164 LRR 2.
FT REPEAT 164 197 LRR 3.
FT REPEAT 197 230 LRR 4.
FT REPEAT 230 263 LRR 5.
FT REPEAT 263 296 LRR 6.
FT REPEAT 296 329 LRR 7.
FT REPEAT 329 362 LRR 8.
FT DOMAIN 469 491 TIR.
FT CARBOHYD 51 51 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 137 137 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 429 429 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 578 578 N-linked (GlcNAc . . .) (Potential).
FT VARIANT 118 118 H -> Y (in dbSNP:5743612).

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FT FT CONFLICT 80 80 /FtId=VAR_018474.
FT FT CONFLICT 182 182 R -> T (in Ref. 2).
FT FT CONFLICT 228 228 E -> G (in Ref. 3).
FT FT CONFLICT 248 248 N -> S (in Ref. 3).
FT FT CONFLICT 276 276 S -> N (in Ref. 2).
FT FT CONFLICT 296 296 F -> S (in Ref. 3).
FT FT CONFLICT 602 602 I -> S (in Ref. 2).
FT FT STRAND 628 628
FT FT TURN 629 630
FT FT STRAND 631 633
FT FT STRAND 637 642
FT FT HELIX 645 653
FT FT TURN 654 654
FT FT HELIX 655 660
FT FT TURN 661 663
FT FT STRAND 666 667
FT FT TURN 669 672
FT FT TURN 675 676
FT FT STRAND 677 677
FT FT HELIX 679 689
FT FT STRAND 690 698
FT FT HELIX 699 704
FT FT TURN 705 705
FT FT STRAND 706 706
FT FT HELIX 707 712
FT FT TURN 713 714
FT FT STRAND 715 715
FT FT STRAND 719 719
FT FT STRAND 721 722
FT FT STRAND 724 732
FT FT HELIX 736 738
FT FT STRAND 739 739
FT FT TURN 741 742
FT FT HELIX 744 751
FT FT TURN 752 752
FT FT STRAND 756 757
FT FT STRAND 760 761
FT FT HELIX 762 764
FT FT STRAND 765 766
FT FT HELIX 767 777
FT FT STRAND 778 778
FT FT SEQUENCE 786 AA; 1406C60FB5847F58 CRC64;
SQ
OY 1 FRDPDY 6
Db 289 FRDPDY 294
Query Match 100.0%; Score 36; DB 1; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 9
O32MK3 HUMAN PRELIMINARY; PRT; 786 AA.
ID O32MK3 HUMAN
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
GN Toll-like receptor 1.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxId=9606;
OX [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
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CC Distributed under the Creative Commons Attribution-NonDerivs License
-----
DR EMBL: BC109094; AA109095.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 786 AA; 90290 MW; 1406C60FB5847F58 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDFDY 6
Db 289 FRDFDY 294

RESULT 10
Q32MK4 HUMAN PRELIMINARY; PRT; 786 AA.
ID Q32MK4;
AC Q32MK4;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
OX
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
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-----
DR EMBL: BC109093; AA109094.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 786 AA; 90291 MW; 1BFCC5E42EA5242 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FRDFDY 6
Db 289 FRDFDY 294

RESULT 11
Q5FMG5 HUMAN PRELIMINARY; PRT; 786 AA.
ID Q5FMG5;
AC Q5FMG5;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Toll-like receptor 1.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
OX
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lymph;
RA Director MGC Project;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:09:23 / Search time 24 Seconds
(without alignments)
24.054 Million cell updates/sec

Title: 09937009-A

Perfect score: 36

Sequence: 1 finddy 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	36	100.0	585	2	G96995
2	36	100.0	786	2	T08664
3	36	100.0	984	2	S67527
4	33	91.7	168	2	T18236
5	33	91.7	210	2	G64614
6	33	91.7	235	2	D71901
7	33	91.7	434	2	S42676
8	33	91.7	511	2	AE2078
9	33	91.7	993	2	C31915
10	32	88.9	281	2	PC4220
11	32	88.9	889	2	JC7083
12	32	88.9	946	2	UC2130
13	32	88.9	1120	2	S67208
14	32	88.9	1849	2	T00415
15	31	86.1	238	2	T24899
16	31	86.1	247	1	KYHUCM
17	31	86.1	525	2	T13926
18	31	86.1	1428	2	G64363
19	30	83.3	222	2	T23435
20	30	83.3	298	2	H97089
21	30	83.3	363	2	F69325
22	30	83.3	384	2	D75638
23	30	83.3	384	2	T23604
24	30	83.3	390	1	B86790
25	30	83.3	402	2	G58477
26	30	83.3	408	2	G96500
27	30	83.3	425	2	E69551
28	30	83.3	446	2	A84940
29	30	83.3	446	2	A84940

30	30	83.3	462	2	T05362	glycine hydroxymet
31	30	83.3	491	2	A11759	hypothetical prote
32	30	83.3	515	2	F70128	transcription term
33	30	83.3	644	2	T10403	p74 protein - Orgy
34	30	83.3	645	2	WMNV74	p74 protein - Auto
35	30	83.3	645	2	C72867	occlusion-derived
36	30	83.3	645	2	S29849	gene p74 protein -
37	30	83.3	655	2	G70900	probable p74 prot
38	30	83.3	681	2	E88158	protein C17G10.4c
39	30	83.3	708	2	T34098	hypothetical prote
40	30	83.3	715	2	B83222	regulatory protein
41	30	83.3	775	2	T45238	probable transfe
42	30	83.3	789	2	A70868	probable p18B2 - M
43	30	83.3	1042	1	GBRCE	beta-galactosidase
44	30	83.3	1042	2	E85968	evolved beta-D-gal
45	30	83.3	1042	2	F91123	evolved beta-D-gal

ALIGNMENTS

RESULT 1

G96995
ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G96995
R:Noiling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c
A:Reference number: A96900; MIMD:21359325; PMID:21359325
A:Accession: G96995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <KUR>
A:Cross-references: UNIPROT:Q97KY8; UNIPARC:UPI00000C9F97; GB:AE001437; PIDN:AAK78754.1;
A:Experimental source: Clostridium acetobutylicum ATCC6824
C:Genetics:
A:Gene: CAC0778

Query Match 100.0%; Score 36; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
Db 54 FRDFDY 59

RESULT 2

T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C:Species: Homo sapiens (man)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08664
R:Poustra, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16466
A:Accession: T08664
A:Molecule type: mRNA
A:Residues: 1-786 <POU>
A:Cross-references: UNIPROT:Q15399; UNIPARC:UPI000016AC46; EMBL:AL050262
A:Experimental source: fetal brain; clone DKFZp547I0610
C:Genetics:
A:Note: DKFZp547I0610.1

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRDFDY 6
|||||

Db 289 FRDPDY 294

RESULT 3

367527

protein kinase (EC 2.7.1.-) PKR2 - human

C/Species: Homo sapiens (man)

C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Oct-2004

C/Accession: S67527; 167464

R/Palmer, R.H.; Ridden, J.; Parker, P.J.

Eur. J. Biochem. 227, 344-351, 1995

A/Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela

A/Reference number: 153327; MUID:95154310; PMID:7851406

A/Accession: S67527

A/Molecule type: mRNA

A/Residues: 1-984 <PAL>

A/Cross-references: UNIPROT:Q16513; UNIPARC:UPI000004D291; EMBL:S75548; NID:g914099; PII

A/Experimental source: fetal brain

A/Accession: 167464

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-984 <RES>

A/Cross-references: UNIPARC:UPI000004D291; GB:S75548; NID:g914099; PIDN:AMB33346.1; PID

C/Keywords: ATP; phosphotransferase

F/555-916/Domain: protein kinase homology <KIN>

F/663-671/Region: protein kinase ATP-binding motif

F/686/Active site: Lys #status predicted

Query Match 100.0%; Score 36; DB 2; Length 984;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6

Db 974 FRDPDY 979

RESULT 4

T18236

protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - yeast (Candida albicans

C/Species: Candida albicans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18236

R/Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL data library, November 1998

A/Reference number: Z18831

A/Accession: preliminary; translated from GB/EMBL/DBJ

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalek, H.G.; Glodek, A.; McKenney

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hays, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: C64614

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-210 <TOM>

A/Cross-references: UNIPROT:Q25450; UNIPARC:UPI00000D313A; GB:AE000588; GB:AE000511; NID

C/Genetics: TTT

A/Start codon: TTT

C/Superfamily: Molybdopterin biosynthesis protein moeb

Query Match 91.7%; Score 33; DB 2; Length 210;

Best Local Similarity 83.3%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6

Db 92 FRDPDY 97

RESULT 6

D71901

hypothetical protein jhp0692 - *Helicobacter pylori* (strain J99)

C/Species: *Helicobacter pylori*

C/Variety: strain J99

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2004

C/Accession: D71901

R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A/Reference number: A71800; MUID:99120557; PMID:9923682

A/Accession: D71901

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-235 <ARN>

A/Cross-references: UNIPROT:Q9ZL68; UNIPARC:UPI00000D722E; GB:AE001500; GB:AE001439; NID

C/Superfamily: Molybdopterin biosynthesis protein moeb

C/Genetics:

A/Status: preliminary

Query Match 91.7%; Score 33; DB 2; Length 235;

Best Local Similarity 83.3%; Pred. No. 21;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6

Db 105 FRDPDY 110

RESULT 7

S42676

KES1 protein - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: protein P2614; protein YPL145C

C/Species: *Saccharomyces cerevisiae*

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S42676; S65156; S69042; S69454

R/Jiang, B.; Brown, J.L.; Sheraton, J.; Fortin, N.; Bussey, H.

Yeast 10, 341-353, 1994

A/Title: A new family of yeast genes implicated in ergosterol synthesis is related to the

A/Reference number: S42676; MUID:94287711; PMID:8017104

A/Accession: S42676

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-434 <DIA>

A/Cross-references: UNIPROT:P35844; UNIPARC:UPI000012DD9B; GB:U03913; NID:9433362; PIDN:

R/Parnelle, B.; Cosser, F.; Goffeau, A.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S65154
A:Accession: S65156
A:Molecule type: DNA
A:Residues: 1-434 <PWR>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:Z73501; NID:G1370309; PID:G247042; PID:G
A:Experimental source: strain S28C (AB972)
R:Hall, J.; Depaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm.
A:Reference number: S69040
A:Accession: S69042
A:Molecule type: DNA
A:Residues: 1-434 <HML>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:U43703; NID:G1244769; PID:G1244772; MIPS
R:Purnelle, B.; Combiez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
ogues to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
A:Reference number: S69428
A:Accession: S69454
A:Molecule type: DNA
A:Residues: 1-434 <PPW>
A:Cross-references: UNIPARC:UPI000012DD9B; EMBL:X96770; NID:G1403537; PID:G239051; PID:G
C:Genetics:
A:Gene: SGD:KES1
A:Cross-references: SGD:S0006066; MIPS:YPL145C
A:Map position: 16L

Query Match 91.7%; Score 33; DB 2; Length 434;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 FRPDFY 6
Db 362 FKPDFY 367

RESULT 8
AE2078
Leitchrome-10 receptor [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2078
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasa moto, S.; Watanabe, A.; Itiguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:2159585; PMID:11759840
A:Accession: AE2078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <KUR>
A:Cross-references: UNIPROT:Q8YV02; UNIPARC:UPI00000CE34D; GB:BA000019; PIDN:BA873878.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2179

Query Match 91.7%; Score 33; DB 2; Length 511;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 FRPDFY 6
Db 304 FRPDFY 309

RESULT 9
C31915
lanthibiotic nisin biosynthesis protein nisB - *Lactococcus lactis*
N:Alternate names: probable membrane-associated protein A
C:Species: *Lactococcus lactis*
C:Date: 21-May-1990 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: S36735; C31915; C48951; C45821; B43743; S36985
R:Kuipers, O.P.; Beertshuyzen, M.M.; Sijzen, R.J.; de Vos, W.M.
Eur. J. Biochem. 216, 281-291, 1993
A:Title: Characterization of the nisin gene cluster nisAB/CIPR of *Lactococcus lactis*. Re
A:Reference number: S36734; MUID:93373937; PMID:7689965
A:Accession: S36735
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-634, 'T', 636-993 <KUI>
A:Cross-references: UNIPROT:P20103; UNIPARC:UPI000017AC47; GB:L16226; NID:G400365
R:Buchanan, G.W.; Banerjee, S.; Hansen, J.N.
J. Biol. Chem. 263, 16260-16266, 1988
A:Title: Structure, expression, and evolution of a gene encoding the precursor of nisin,
A:Reference number: A92679; MUID:89034093; PMID:3141403
A:Accession: C31915
A:Molecule type: DNA
A:Residues: 1-63 <BUC>
A:Cross-references: UNIPARC:UPI0000170131; GB:J04057; NID:G153816; PIDN:AAA88607.1; PID:
R:Engelke, G.; Gutowski-Eckel, Z.; Hammelmann, M.; Entian, K.D.
Appl. Environ. Microbiol. 58, 3730-3743, 1992
A:Title: Biosynthesis of the lantibiotic nisin: genomic organization and membrane local
A:Reference number: A48951; MUID:93128945; PMID:1482192
A:Accession: C48951
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'C', 20-655, 'K', 657-894, 'T', 896-993 <ENG>
A:Cross-references: UNIPARC:UPI00001301CE; GB:X68307; GB:S52234; NID:G44040; PIDN:CAA483
A:Experimental source: strain 6F3
A:Note: sequence extracted from NCBI backbone (NCBI:122292, NCBI:122296)
R: Dodd, H.M.; Horn, N.; Gasson, M.J.
J. Gen. Microbiol. 136, 555-566, 1990
A:Title: Analysis of the genetic determinant for production of the peptide antibiotic ni
A:Reference number: A45821; MUID:90362041; PMID:2118169
A:Accession: C45821
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <DOD>
A:Cross-references: UNIPARC:UPI000017AC48; GB:M79445
R:Steen, M.T.; Chung, Y.J.; Hansen, J.N.
Appl. Environ. Microbiol. 57, 1181-1188, 1991
A:Title: Characterization of the nisin gene as part of a polycistronic operon in the chr
A:Reference number: A43743; MUID:91282469; PMID:1905517
A:Accession: B43743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840, 'VPLIKFQICLH' <STB>
A:Cross-references: UNIPARC:UPI000016F8B1; EMBL:M65089; NID:G149447; PIDN:AAV7039.1; PI
A:Note: the authors translated the codon AGC for residue 635 as Thr
C:Genetics:
A:Gene: nisB
C:Keywords: antibiotic biosynthesis; transmembrane protein
F:838-851/Domain: transmembrane #status predicted <TM>

Query Match 91.7%; Score 33; DB 2; Length 993;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 FRPDFY 6
Db 595 YRPDFY 600

RESULT 10
PC4220
protein kinase (EC 2.7.1.37) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Oct-2004
C:Accession: PC4220
R:Batschke, B.; Sundelin, J.
Biochem. Biophys. Res. Commun. 227, 70-76, 1996
A:Title: The mouse genes for the EPI prostanoicd receptor and the PKN protein kinase over
A:Reference number: PC4220; MUID:97011095; PMID:8858105
A:Accession: PC4220

A:Molecule type: DNA
 A:Residues: 1-281 <BAT>
 A:Cross-references: UNIPARC:UPI000017A421; GB:Y07611
 C:Comment: This protein mediates GTPase Rho dependent intracellular signalling.
 C:Genetics:

A:Gene: pgn
 A:introns: 59/2; 80/2; 106/1; 153/3; 189/3; 216/3
 C:Keywords: phosphotransferase
 F:1-213/Domain: protein kinase homology (fragment) <KIN>

Query Match 88.9%; Score 32; DB 2; Length 281;
 Best Local Similarity 83.3%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
 Db 271 FRDFDF 276

RESULT 11

JC7083 protein kinase (EC 2.7.1.37) N beta - human

C:Species: Homo sapiens (man)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
 C/Accession: JC7083
 R:Oishi, K.; Mukai, H.; Shibata, H.; Takahashi, M.; Ona, Y.
 Biochem. Biophys. Res. Commun. 261, 808-814, 1999
 A:title: Identification and characterization of PKM beta, a novel isoform of protein kin
 A:Reference number: JC7083; PMID:99373159; PMID:10441506
 A:Accession: JC7083
 A:Molecule type: mRNA
 A:Residues: 1-889 <OIS>

A:Cross-references: UNIPROT:Q9UM03; UNIPARC:UPI000017A456; DDBJ:AB019692
 C:Keywords: ATP; leucine zipper; phosphotransferase; protein kinase
 F:557-818/Domain: protein kinase homology <KIN>
 F:565-573/Region: protein kinase ATP-binding motif
 F:588/Active site: Lys #status predicted

Query Match 88.9%; Score 32; DB 2; Length 889;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
 Db 676 FRDFDF 881

RESULT 12

JC2130 protein kinase (EC 2.7.1.37) - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
 C/Accession: JC2130
 R:Mukai, H.; Ono, Y.
 Biochem. Biophys. Res. Commun. 199, 897-904, 1994
 A:title: A novel protein kinase with leucine zipper-like sequences: Its catalytic domain
 A:Reference number: JC2129; PMID:94183274; PMID:8135837
 A:Accession: JC2130
 A:Molecule type: mRNA
 A:Residues: 1-946 <MIK>

A:Cross-references: UNIPROT:Q8V1J2; UNIPARC:UPI000017A3DF
 C:Keywords: ATP; leucine zipper; phosphotransferase
 F:39-66/Region: basic
 F:70-290/Region: leucine zipper motif
 F:617-878/Domain: protein kinase homology <KIN>
 F:625-633/Region: protein kinase ATP-binding motif
 F:648/Active site: Lys #status predicted

Query Match 88.9%; Score 32; DB 2; Length 946;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6

Db 936 FRDFDF 941

RESULT 13

S67208

hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein O5648
 C:Species: Saccharomyces cerevisiae
 C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S67208
 R:Ciepluch, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobiasch, E.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67194
 A:Accession: S67208

A:Molecule type: DNA
 A:Residues: 1-1120 <CZI>
 A:Cross-references: UNIPROT:Q08773; UNIPARC:UPI000052F03; EMBL:Z75212; NID:91420670; PII
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:ISW2; MIPS:YOR304w
 A:Cross-references: SGD:S0005831
 A:Map position: 15R
 C:Superfamily: Chromatin remodelling complex ATPase chain ISWI; bromodomain homology

Query Match 88.9%; Score 32; DB 2; Length 1120;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
 Db 528 FRDFEX 533

RESULT 14

T00415 hypothetical protein H_248015.1 - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T00415
 R:Pillon, B.; Nhan, M.; Hawkins, J.; Beck, C.
 submitted to the EMBL Data Library, September 1998
 A:Description: The sequence of Homo sapiens PAC clone 248015.
 A:Reference number: Z14148
 A:Accession: T00415
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1849 <FUI>
 A:Cross-references: UNIPROT:O14572; UNIPARC:UPI0000073A97; EMBL:AC002483; NID:93598729; F
 C:Genetics:
 A:Map position: 13q12-q13
 A>Note: H_248015.1

Query Match 88.9%; Score 32; DB 2; Length 1849;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDFDY 6
 Db 1835 FRDFDF 1840

RESULT 15

T24899

hypothetical protein T13H5.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T24899
 R:Lightning, J.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: Z19950
 A:Accession: T24899
 A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
A:Residues: 1238 <RTL>
A:Cross-references: UNIPROT:Q22470; UNIPARC:UPI00000748F0; EMBL:Z66524; PIDN:CAA91421.1
A:Experimental source: clone T13H5
C:Genetics:
A:Gene: CESP:T13H5.5
A:Map position: 2
C;introns: 33/3; 65/1; 84/3; 111/3
C;superfamily: Caenorhabditis elegans hypothetical protein T13H5.5

Query Match 86.1%; Score 31; DB 2; Length 238;
Best local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
||:||||
Db 174 FRNPDY 179

Search completed: June 14, 2006, 02:17:19
Job time : 27 secs

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CC -----
DR EMBL: BC089403; AAH89403.1; -; mRNA.
DR SMR: Q5FWG5; 625-785.
DR Ensemble1: ENSG00000174125; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR004075; IL1_rcpt_1.
DR InterPro: IPR003016; Lipoyl_BS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_CYP.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRCT; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO0019; LEURICRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 786 AA; 90267 MW; 6B9B673FEE47BF3A CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 12
O6F164_HUMAN PRELIMINARY; PRT; 786 AA.
AC O6F164;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE TLR1 protein.
GN Name=TLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: CR333562; CAG38593.1; -; mRNA.
DR SMR: Q6F164; 625-785.
DR Ensemble1: ENSG00000174125; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR004075; IL1_rcpt_1.
DR InterPro: IPR003016; Lipoyl_BS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_CYP.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01463; LRCT; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO1537; INTRLNRI1F.

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DR PRINTS: PRO0019; LEURICRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00189; LIPOYL; UNKNOWN_1.
DR PROSITE: PS50104; TIR; 1.
SQ SEQUENCE 786 AA; 90163 MW; DB6B54E6840092B4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 289 FRDPDY 294

RESULT 13
Q4LDR7_PIG PRELIMINARY; PRT; 796 AA.
AC Q4LDR7;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Toll-like receptor 1.
GN Name=TLR1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxId=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine.
RA Shinkai H., Muneta Y., Suzuki K., Eguchi-Ogawa T., Awata T.,
RA Denishi H.;
RT "Complete nucleotide sequence in the porcine genomic region containing
RT Toll-like receptors 1, 6, and 10 genes and their expression
RT analysis."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AB219564; BAB06146.1; -; mRNA.
DR SMR: Q4LDR7; 629-789.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro: IPR004075; IL1_rcpt_1.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_C.
DR InterPro: IPR003591; LRR_CYP.
DR InterPro: IPR000157; TIR.
DR Pfam: PF00560; LRR_1; 7.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRLNRI1F.
DR PRINTS: PRO0019; LEURICRPT.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 796 AA; 90967 MW; 396C3D6B9B99442C4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 796;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRDPDY 6
Db 293 FRDPDY 298

RESULT 14
O59H19_PIG

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ID 059H19_PIG PRELIMINARY; PRT; 796 AA.
AC 059H19;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
GN TOLL-like receptor 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shinkai H., Uenishi H.;
RT "Coding sequence of porcine TLR1."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Shinkai H., Uenishi H.;
RT "Nucleotide sequence of porcine genomic region containing TLR1, TLR6
RT and TLR10."
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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DR EMBL; AB208695; BAD91798.1; -; Genomic_DNA.
DR EMBL; AB210286; BAD93714.1; -; Genomic_DNA.
DR SMR; Q59H19; 629-789.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR004075; IL1_rcpt_1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRNLNRI1F.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR Receptor.
SQ SEQUENCE 796 AA; 90948 MW; 396C38C261A642C4 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 796;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 293 FRDPDY 298

RESULT 15
QARZS3_TETNG
ID QARZS3_TETNG PRELIMINARY; PRT; 966 AA.
AC QARZS3;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE 21-FEB-2006, entry version 6.
DE Chromosome 18 SCARF4786, whole genome shotgun sequence. (Fragment).
GN OxFNames=GSTENG00026354001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segutens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellio V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brotier P., Coultanceau J.-P., Gouzy J.,
RA Parra G., Vardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Valtier G., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -----
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CC -----
DR EMBL; CAE01014786; CAG06109.1; -; Genomic_DNA.
DR SMR; QARZS3; 119-184.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000861; REM_Typ_rho_bd.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02185; HR1; 3.
DR Pfam; PF00069; Kinase_C; 1.
DR Pfam; PF00433; Kinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00742; Hr1; 3.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 966
SQ SEQUENCE 966 AA; 109614 MW; F74D1C73A072A4FC CRC64;

Query Match 100.0%; Score 36; DB 2; Length 966;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRDPDY 6
DB 956 FRDPDY 961

Search completed: June 14, 2006, 02:16:26

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Job time : 223 secs

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7	35	100.0	7	ADS91353
8	35	100.0	9	AAV93661
9	35	100.0	10	AAW51726
10	35	100.0	10	AAW51737
11	35	100.0	10	AD074882
12	35	100.0	11	AAV44724
13	35	100.0	11	AAV59262
14	35	100.0	11	ADR06310
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70	35	100.0	12	AAW34387
71	35	100.0	12	AAW34387
72	35	100.0	12	AAW34387
73	35	100.0	12	AAW34387
74	35	100.0	12	AAW34387
75	35	100.0	12	AAW34387
76	35	100.0	12	AAW34387
77	35	100.0	12	AAW34387
78	35	100.0	12	AAW34387
79	35	100.0	12	AAW34387
80	35	100.0	12	AAW34387
81	35	100.0	12	AAW34387
82	35	100.0	12	AAW34387
83	35	100.0	12	AAW34387
84	35	100.0	12	AAW34387
85	35	100.0	12	AAW34387
86	35	100.0	12	AAW34387
87	35	100.0	12	AAW34387
88	35	100.0	12	AAW34387
89	35	100.0	12	AAW34387
90	35	100.0	12	AAW34387
91	35	100.0	12	AAW34387
92	35	100.0	12	AAW34387
93	35	100.0	12	AAW34387
94	35	100.0	12	AAW34387
95	35	100.0	12	AAW34387
96	35	100.0	12	AAW34387
97	35	100.0	12	AAW34387
98	35	100.0	12	AAW34387
99	35	100.0	12	AAW34387
100	35	100.0	12	AAW34387

24	35	100.0	14	9	AED01166
25	35	100.0	14	9	AED01161
26	35	100.0	14	9	AED01158
27	35	100.0	15	8	AAM34389
28	35	100.0	15	8	ADT92476
29	35	100.0	16	8	ADJ03822
30	35	100.0	16	9	AED01147
31	35	100.0	20	7	ADJ12327
32	35	100.0	22	6	ABR57449
33	35	100.0	22	7	ABD92662
34	35	100.0	28	3	AAB13392
35	35	100.0	31	7	ABR98382
36	35	100.0	31	8	ADJ38880
37	35	100.0	31	8	ABR9831
38	35	100.0	31	8	ADJ38879
39	35	100.0	31	9	ABR98933
40	35	100.0	31	9	ADJ38881
41	35	100.0	33	8	ADR06326
42	35	100.0	33	8	ADR06539
43	35	100.0	33	6	ABR57469
44	35	100.0	33	7	ABR57459
45	35	100.0	36	9	AED54161

ALIGNMENTS

RESULT 1
ABR57446
ID ABR57446 standard; peptide; 6 AA.

AC ABR57446;

DT 15-SEP-2003 (first entry)

PKB activity modulating peptide #10.

KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;

KW nootropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;

KW neurodegeneration.

OS Synthetic.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
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92	92	92
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94	94	94
95	95	95
96	96	96
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98	98	98
99	99	99
100	100	100

FT /note= "phosphoserine"

PN WO2003016516-A2.

PD 27-FEB-2003

PF 14-AUG-2002; 2002WO-GB003735.

PR 14-AUG-2001; 2001GB-00019860.

xx

PA (CANC-) CANCER RES INST.

PI Barford D, Yang J, Hemmings BA, Cron PD;

WPI; 2003-268328/26.

PT New crystal of protein kinase B beta, useful for activating protein

PT or a tetragonal space group.

PS Claim 32; Page 265; 284pp; English.

CC The present invention describes a crystal of protein kinase B beta
CC (PKBbeta) comprising: (a) a tetragonal

CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
 CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
 CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
 CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
 CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
 CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
 CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
 CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
 CC the specification. (1) has cytosstatic, antidiabetic, vasotropic,
 CC neurotropic and neuroprotective activities, and can be used in gene
 CC therapy. The crystal of PEBbeta, and methods from the present invention,
 CC are useful in activating protein kinases, particularly AGC kinases, for
 CC identifying modulators of protein kinase activity, and for structural
 CC analysis of other protein kinases. The crystal may also be used in
 CC manufacturing a medicament for treating cancers, diabetes, erectile
 CC dysfunction or neurodegeneration. The present sequence represents a
 CC peptide which can be used in a method from the present invention to
 CC modulate PKB activity

CC Sequence 6 AA;

Query Match 100.0%; Score 35; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 DB 1 PPOFSY 6

RESULT 2
 ABU64720
 ID ABU64720 standard; peptide; 6 AA.

AC ABU64720;

DT 13-MAY-2003 (first entry)

XX Motif-specific and context-independent antibody peptide antigen #143.

XX Motif-specific antibody;
 KM context-independent antibody. enzyme substrate identification;
 KM modification state detection; enzyme inhibition; enzyme activation;
 KM protein level profile; post-translation modification; phosphochreonine;
 KM phosphoserine; phosphotyrosine; acetyl-lysine; nitrotyrosine;
 KM kinase consensus substrate motif; protein binding motif.

OS Homo sapiens.
 OS Synthetic.

PN US2002168684-A1.

XX 14-NOV-2002.

PD 13-NOV-2001; 2001US-00014485.

PR 04-SEP-1998; 98US-00148712.

PR 24-MAR-2000; 2000US-00535364.

PA (COMB/) COMB M J.
 PA (TANY/) TAN Y.
 PA (ZHAN/) ZHANG H.

PI Comb MJ, Tan Y, Zhang H;

DR WPI; 2003-298726/29.

PT Producing motif-specific, context-independent antibody recognizing motif-
 PT containing proteins, using a degenerate peptide library having target
 PT motifs with invariant amino acids flanked by degenerate amino acids, as
 PT antigens.

PS Example 14; Fig 27; 86pp; English.

XX The invention describes a method of producing a motif-specific, context-
 CC independent antibody (1) that recognises several peptides or proteins
 CC within the genome that contain motifs. The method is useful for: (1)
 CC identifying an unknown substrate of an enzyme, which involves generating
 CC at least one (1) which recognizes a motif common to several substrate of
 CC the enzyme with a genome; (2) detecting the modification state of a
 CC target substrate that contains a motif common to several substrates of an
 CC enzyme within a genome; (3) screening a drug for the inhibition or
 CC activation of enzyme activity on at least one substrate that contains a
 CC motif common to several substrates of the enzyme within a genome; (4)
 CC identifying an enzyme which modifies a known substrate that contains a
 CC motif common to several substrates of the enzyme within a genome; (5)
 CC profiling protein levels or post-translation modifications in a cell or
 CC tissue on a genome wide scale; (6) profiling drug-induced changes in
 CC protein levels or post-translation modifications in a cell or tissue on a
 CC genome wide scale. The motif is selected from single phosphotyrosine, a
 CC single phosphoserine, a single phosphotyrosine, a single acetyl-lysine,
 CC and a single nitrotyrosine, and comprises all or part of kinase consensus
 CC substrate motif or a protein binding motif. This is the amino acid
 CC sequence of a peptide used in the creation of a motif-specific, context-
 CC independent antibody

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 DB 1 PPOFSY 6

RESULT 3
 ADJ38822
 ID ADJ38822 standard; peptide; 6 AA.

AC ADJ38822;

DT 06-MAY-2004 (first entry)

XX PKB-gamma AGC hydrophobic motif peptide.

XX phosphoinositide dependent protein kinase 1; PKR1; molecular modelling;
 KM protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 KM insulin signalling pathway; signalling; crystalline form;
 KM protein co-ordinate data; three-dimensional structure; antifungal;
 KM antidiabetic; cardiant; cytosstatic; cerebroprotective; vasotropic;
 KM anorectic; protein kinase modulator; cancer; diabetes; obesity;
 KM apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 KM neural injury.

OS Synthetic.

PN WO2003104481-A2.

PD 18-DEC-2003.

PR 09-JUN-2003; 2003WO-GB002509.

PR 08-JUN-2002; 2002GB-00013186.

PA (UYDU-) UNIV DUNDEE.

PI Alessi D, Biondi R, Komander D, Van AD;

DR WPI; 2004-062373/06.

PT Selecting/designing compound for modulating activity of phosphoinositide
 PT dependent protein kinase 1 by using molecular modelling to select/design
 PT compound predicted to interact with protein kinase catalytic domain.

PS Disclosure; Page 16; 383pp; English.

XX The present invention describes a method (M1) for selecting or designing
CC a compound for modulating the activity of phosphoinositide dependent
CC protein kinase 1 (PDK1) comprising using molecular modelling means to
CC select or design a compound that is predicted to interact with the
CC protein kinase catalytic domain of PDK1, and selecting a compound that is
CC predicted to interact with the protein kinase catalytic domain. Also
CC described: (1) selecting or designing (M2) a compound for modulating the
CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
CC kinase having a hydrophobic pocket in the position equivalent to the
CC hydrophobic pocket of human PDK1 that is defined by residues including
CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
CC PDK1 and further having a phosphate binding pocket in the position
CC equivalent to the phosphate binding pocket of human PDK1 that is defined
CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
CC (M3) the activation state of a structure for a protein kinase; (3) a
CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a
CC host cell (III) comprising (II); (6) identifying (M4) a compound that
CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein
CC kinase mutated at the phosphate binding site, or vice versa; (8) a
CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of
CC a medicament for the treatment of a patient in need of modulation of
CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
CC p70 S6 kinase, for example insulin signalling pathway and/or
CC PKA1/SGK/PRK/p70 S6 kinase/PRK2/PKC signalling; and (11) a
CC crystalline form (VI) of polypeptide as defined in (M1). (I) has
CC antifungal, antidiabetic, cardiant, cyrostatic, cerebroprotective,
CC vasotropic and anorectic activities, and can be used as a modulator of
CC protein kinase. (V) is useful for modulating the ability of protein
CC kinase to phosphorylate different substrates, e.g., different naturally
CC occurring polypeptides, to different extents. (V) inhibits or increases
CC the activity of protein kinase. The protein structures e.g., the co-
CC ordinates as provided in the specification are useful for designing
CC reagent useful in drug designing assays or characterisation of protein
CC kinase activity or regulation. (V) capable of producing the activity of
CC PKC, e.g., PKC beta, PKA1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
CC useful in treating cancer. (V) capable of increasing the activity of
CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
CC or may be useful in inhibiting apoptosis, thus useful in treating
CC diseases in which apoptosis is involved e.g., mechanical (including heat)
CC tissue injury or ischaemia disease such as stroke, myocardial infarction
CC and neural injury. (V) is useful as an antifungal agent. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 6 AA:

Query Match 100.0%; Score 35; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. NO. 2.1e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
| | | | |
Db 1 FPOFSY 6

RESULT 4
ADJ38820
ID ADJ38820 standard; peptide; 6 AA.

XX ADJ38820;

XX 06-MAY-2004 (first entry)

XX PKA-alpha AGC hydrophobic motif peptide.

XX phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;

XX protein kinase; catalytic domain; enzyme; hydrophobic pocket;

KW insulin signalling pathway; signalling; crystalline form;

KW protein co-ordinate data; three-dimensional structure; antifungal;

KW antidiabetic; cardiant; cyrostatic; cerebroprotective; vasotropic;
KW anorectic; protein kinase modulator; cancer; diabetes; obesity;
KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
KW neural injury.

XX Synthetic.

XX WO2003104481-A2.

XX 18-DEC-2003.

XX 09-JUN-2003; 2003WO-GB002509.

XX 08-JUN-2002; 2002GB-00013186.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R, Komander D, Van AD;

XX WPI: 2004-062373/06.

PS Selecting/designing compound for modulating activity of phosphoinositide
PT dependent protein kinase 1 by using molecular modelling to select/design
PT compound predicted to interact with protein kinase catalytic domain.
XX

PS Disclosure; Page 16; 383pp; English.

XX The present invention describes a method (M1) for selecting or designing
CC a compound for modulating the activity of phosphoinositide dependent
CC protein kinase 1 (PDK1) comprising using molecular modelling means to
CC select or design a compound that is predicted to interact with the
CC protein kinase catalytic domain of PDK1, and selecting a compound that is
CC predicted to interact with the protein kinase catalytic domain. Also
CC described: (1) selecting or designing (M2) a compound for modulating the
CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
CC kinase having a hydrophobic pocket in the position equivalent to the
CC hydrophobic pocket of human PDK1 that is defined by residues including
CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
CC PDK1 and further having a phosphate binding pocket in the position
CC equivalent to the phosphate binding pocket of human PDK1 that is defined
CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
CC (M3) the activation state of a structure for a protein kinase; (3) a
CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a
CC host cell (III) comprising (II); (6) identifying (M4) a compound that
CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein
CC kinase mutated at the phosphate binding site, or vice versa; (8) a
CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of
CC a medicament for the treatment of a patient in need of modulation of
CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
CC p70 S6 kinase, for example insulin signalling pathway and/or
CC PDK1/SGK/PRK/p70 S6 kinase/PRK2/PKC signalling; and (11) a
CC crystalline form (VI) of polypeptide as defined in (M1). (I) has
CC antifungal, antidiabetic, cardiant, cyrostatic, cerebroprotective,
CC vasotropic and anorectic activities, and can be used as a modulator of
CC protein kinase. (V) is useful for modulating the ability of protein
CC kinase to phosphorylate different substrates, e.g., different naturally
CC occurring polypeptides, to different extents. (V) inhibits or increases
CC the activity of protein kinase. The protein structures e.g., the co-
CC ordinates as provided in the specification are useful for designing
CC reagent useful in drug designing assays or characterisation of protein
CC kinase activity or regulation. (V) capable of producing the activity of
CC PKC, e.g., PKC beta, PKA1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is
CC useful in treating cancer. (V) capable of increasing the activity of
CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
CC or may be useful in inhibiting apoptosis, thus useful in treating
CC diseases in which apoptosis is involved e.g., mechanical (including heat)
CC tissue injury or ischaemia disease such as stroke, myocardial infarction
CC and neural injury. (V) is useful as an antifungal agent. The present
CC sequence is used in the exemplification of the present invention.

SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 |||||
 1 PPOFSY 6

Db 1 PPOFSY 6

RESULT 5
 ADS91353
 ID ADS91353 standard; peptide; 6 AA.
 XX
 AC ADS91353;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE PKB-beta AGC hydrophobic motif peptide.
 XX
 KM phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;
 KM protein kinase; catalytic domain; enzyme; hydrophobic pocket;
 KM insulin signalling pathway; signalling; crystalline form;
 KM protein co-ordinate data; three-dimensional structure; antifungal;
 KM antidiabetic; cardiant; cytosolic; cerebroprotective; vasotrophic;
 KM anorectic; protein kinase modulator; cancer; diabetes; obesity;
 KM apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;
 KM neural injury.
 XX
 OS Synthetic.
 XX
 PN MO2003104481-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 09-JUN-2003; 2003WO-GB002509.
 XX
 PR 08-JUN-2002; 2002GB-00013186.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Alessi D, Biondi R, Komander D, Van AD;
 XX
 DR WPI; 2004-062373/06.
 XX
 PT Selecting/designing compound for modulating activity of phosphoinositide
 PT dependent protein kinase 1 by using molecular modelling to select/design
 PT compound predicted to interact with protein kinase catalytic domain.
 XX
 PS Disclosure; Page 16; 383pp; English.
 XX
 CC The present invention describes a method (M1) for selecting or designing
 CC a compound for modulating the activity of phosphoinositide dependent
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to
 CC select or design a compound that is predicted to interact with the
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is
 CC predicted to interact with the protein kinase catalytic domain. Also
 CC described: (1) selecting or designing (M2) a compound for modulating the
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein
 CC kinase having a hydrophobic pocket in the position equivalent to the
 CC hydrophobic pocket of human PDK1 that is defined by residues including
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human
 CC PDK1 and further having a phosphate binding pocket in the position
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing
 CC (M3) the activation state of a structure for a protein kinase; (3) a
 CC mutated protein kinase (1); (4) a polynucleotide (II) encoding (1); (5) a
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);
 CC or (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1
 CC or (1) or an antibody reactive with PDK1 or (1) but not with the protein
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a

CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),
 CC (1), (II) in medicine; (10) use of (V), (1), (II) for the manufacture of
 CC a medicament for the treatment of a patient in need of modulation of
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or
 CC p70 S6 kinase, for example insulin signalling pathway and/or
 CC PDK1/PDK2/SGK/PKB/p70 S6 kinase/PKC2/SGK signalling; and (11) a
 CC crystalline form (VI) of polypeptide as defined in (M1). (1) has
 CC antifungal, antidiabetic, cardiant, cytosolic, cerebroprotective,
 CC vasotrophic and anorectic activities, and can be used as a modulator of
 CC protein kinase. (V) is useful for modulating the ability of protein
 CC kinase to phosphorylate different substrates, e.g., different naturally
 CC occurring polypeptides, to different extents. (V) inhibits or increases
 CC the activity of protein kinase. The protein structures e.g., the co-
 CC ordinates as provided in the specification are useful for designing
 CC reagent useful in drug designing assays or characterisation of protein
 CC kinase activity or regulation. (V) capable of producing the activity of
 CC PKC, e.g., PKC beta, PKA or PKC2, PDK1, PKB, SGK or p70 S6 kinase, is
 CC useful in treating cancer. (V) capable of increasing the activity of
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity
 CC or may be useful in inhibiting apoptosis, thus useful in treating
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction
 CC and neural injury. (V) is useful as an antifungal agent. The present
 CC sequence is used in the exemplification of the present invention.
 XX

SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
 |||||
 1 PPOFSY 6

Db 1 PPOFSY 6

RESULT 6
 ADS91353
 ID ADS91353 standard; peptide; 7 AA.
 XX
 AC ADS91353;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Protein kinase B alpha (PKBalpha) phosphorylated hydrophobic motif.
 XX
 KM AGC protein kinase; AGC protein kinase modulator; truncated AGC kinase;
 KM mutated AGC kinase; cytosolic; antineoplastic; antidiabetic;
 KM anorectic; abnormal cell proliferation; abnormal apoptosis; cancer;
 KM inflammation; diabetes; obesity; apoptosis inhibitor;
 KM protein kinase B alpha; PKBalpha; phosphorylated hydrophobic motif.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5 /note="phosphoserine"
 XX
 PN MO2004035811-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 14-OCT-2003; 2003WO-GB004446.
 XX
 PR 14-OCT-2002; 2002GB-00023893.
 XX
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Biondi RM, Frodin M, Antal TL;
 XX
 DR WPI; 2004-357223/33.
 XX
 PT Identifying AGC protein kinase modulators, for use in therapy, comprises

PT detecting the effect of a test agent on a polypeptide comprising a kinase
 PT domain of an AGC protein kinase and associated activation loop.

PS Disclosure; Page 15; 65pp; English.

XX The present invention describes a method (M1) for identifying AGC protein
 CC kinase (I) modulators, by: (a) providing a polypeptide comprising a
 CC kinase domain of (I), and associated activation loop which may be a
 CC phosphorylated or unphosphorylated; (b) contacting a test agent (T) and
 CC polypeptide(s) under conditions conducive to allow kinase activity to be
 CC detected in absence of (T); and (c) detecting effect of (T) on kinase
 CC activity. Also described: (1) a truncated AGC kinase polypeptide (II) for
 CC use in (M1); (2) a mutated AGC kinase (III) comprising a mutation in a
 CC kinase domain and/or activation loop in order to reduce binding ability
 CC to the hydrophobic motif for use in (M1); (3) a compound/agent (IV)
 CC identified by (M1) for use in therapy; (4) a phosphorylated peptide
 CC comprising the sequence F/Y-X-X-F/Y-S/T-F in which the S/T residue is
 CC phosphorylated; and (5) a peptide comprising the sequence F/Y-X-X-F/Y-E/D
 CC-F. (I) has cytostatic, antiinflammatory, antidiabetic and anorectic
 CC activities, and can be used as an AGC kinase activity modulator. The
 CC method is useful for identifying agents which modulate AGC protein kinase
 CC activity, such as an activator or inhibitor of AGC protein kinase
 CC activity. (II) is useful in (M1). (III) is useful in (M1). (IV) is useful
 CC for the manufacture of a medicament for use in therapy. (IV) is useful
 CC for treating a subject who requires modulation of (I). (IV) which
 CC inhibits AGC kinase activity is useful or treating diseases associated
 CC with abnormal cell proliferation or apoptosis, such as cancer, or
 CC undesirable inflammation. (IV) which activates or increases AGC kinase
 CC activity is useful for treating diabetes or obesity, or is useful for
 CC inhibiting apoptosis. The phosphorylated peptide is useful for modulating
 CC AGC kinase activity. The unphosphorylated hydrophobic motif peptide, is
 CC capable of inhibiting AGC kinase activity, and for designing new
 CC inhibitory agents. The present sequence represents a protein kinase B
 CC alpha (PKBalpha) phosphorylated hydrophobic motif, which is used in the
 CC exemplification of the present invention.

CC Sequence 7 AA:

Query Match 100.0%; Score 35; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
 |||||
 Db 1 FPOFSY 6

RESULT 7
 AAY93661

ID AAY93661 standard; peptide; 9 AA.

AC AAY93661;

DT 25-SEP-2000 (first entry)

DE PKB-alpha sequence for phosphorylation by protein kinase PDK2.

XX Protein kinase; Pkh1, Pkh2, Ypk1, Yrk2; protein kinase B-alpha;
 KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
 KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
 KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX Homo sapiens.

OS WO200036135-A2.

PN 22-JUN-2000.

PF 14-DEC-1999; 99WO-GB004228.

XX 14-DEC-1998; 98US-0112114P.

PR (MEDI-) MEDICAL RES COUNCIL.

PA (REGC) UNIV CALIFORNIA.

XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;

PI WPI; 2000-442391/38.

PT Screening method identifying compounds which modulate protein kinase
 PT activity for use in treating fungal infections and cancer.

PS Disclosure; Fig 6A; 155pp; English.

XX The present sequence represents a sequence which is phosphorylated by
 CC protein kinase PDK1. The specification describes a screening method to
 CC identify a compound which modulates the activity of protein kinases from
 CC different sources, using host yeast cells. The method is used to identify
 CC a compound which modulates (inhibits) the activity of a protein kinase.
 CC Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, human serum and
 CC glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha
 CC (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used
 CC to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or
 CC p70S6 kinase. Compounds identified by the methods are used to treat
 CC fungal infections e.g. thrush, and to treat cancer. To treat cancer, the
 CC compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds
 CC which activate PKB or PDK1 can be used in the treatment of diabetes or
 CC obesity, and compounds which inhibit a fungal functional homologue of
 CC PDK1 (Pkh1 or Pkh2) or SGK (Ypk1 or Yrk2) can be used as an antifungal
 CC agent to treat Candida infections, e.g. thrush

CC Sequence 9 AA:

Query Match 100.0%; Score 35; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
 |||||
 Db 1 FPOFSY 6

RESULT 8
 AAW51736

ID AAW51736 standard; peptide; 10 AA.

AC AAW51736;

DT 10-SEP-1998 (first entry)

DE Protein kinase RAC-PK/Akt alpha internal fragment.

XX Protein kinase; signalling pathway; antiproliferative; assay;
 KW immunosuppressant agent; activation; mitogen; RSK; FKC-epsilon;
 KW protein kinase C; RAC-PK.

XX Unidentified.

PN WO9818935-A2.

PD 07-MAY-1998.

PF 29-OCT-1997; 97WO-EP005979.

PR 31-OCT-1996; 96US-0030262P.

XX (NOVS) NOVARTIS AG.

PA Thomas G, Kozma S;

PI WPI; 1998-272228/24.

PT New protein kinase related to p70S6k pathway enzymes with threonine 389
 PT replaced - by acidic amino acid, has constitutive activity, used to
 PT identify potential antiproliferative and immunosuppressant agents, also
 PT new dominant negative mutant of this enzyme.

PS Disclosure; Page 5; 39pp; English.

XX This invention relates to a new protein kinase, structurally related to a
XX kinase of the p70S6K signalling pathway. It has the S or T residue
CC homologous to T389 in p70S6K replaced by an acidic amino acid which
CC confers constitutive activity. The new protein kinases are used to
CC identify p70S6K kinases responsible for regulation (especially by
CC phosphorylation) of the p70S6K-related kinase and its direct activation
CC through T229, also to screen for compounds that inhibit kinase activity
CC in the p70S6K pathway. The protein kinases of the p70S6K signalling
CC pathway are used to define this signalling pathway and to block upstream
CC kinases. Mutation of T389 with an acidic amino acid produces a several-
CC fold increase in basal kinase activity while retaining susceptibility to
CC activation. Use of the new protein kinases in assays means that the
CC signal pathway can be kept active without addition of exogenous mitogens
CC or other activators. The present sequence represents an internal fragment
CC of RAC-PK/Akt alpha containing an S residue at position 6 homologous to
CC T389 in p70S6K
XX

XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 35; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 PPOFSY 6
Db 2 PPOFSY 7

RESULT 9
ID AAW51737 standard; peptide; 10 AA.
XX AAW51737;
AC AAW51737;
XX
DT 10-SEP-1998 (first entry)
XX
DE Protein kinase RAC-PK/Akt beta internal fragment.
XX
XX Protein kinase; signalling pathway; antiproliferative; assay;
KM immunosuppressant agent; activation; mitogen; RSK; PKC-epsilon;
KW protein kinase C; RAC-PK.
XX
XX Unidentified.
OS
XX WO9818935-A2.
PN
XX
PD 07-MAY-1998.
PF 29-OCT-1997; 97WO-EP005979.
XX
XX 31-OCT-1996; 96US-0030262P.
XX
XX (NOVS) NOVARTIS AG.
PA
XX Thomas G, Kozma S;
PI
XX WPI; 1998-272228/24.
DR
XX

PT New protein kinase related to p70S6K pathway enzymes with threonine 389
PT replaced - by acidic amino acid, has constitutive activity, used to
PT identify potential antiproliferative and immunosuppressant agents, also
PT new dominant negative mutant of this enzyme.
XX
XX
PS Disclosure; Page 5; 39pp; English.
XX
XX This invention relates to a new protein kinase, structurally related to a
CC kinase of the p70S6K signalling pathway. It has the S or T residue
CC homologous to T389 in p70S6K replaced by an acidic amino acid which
CC confers constitutive activity. The new protein kinases are used to
CC identify p70S6K kinases responsible for regulation (especially by
CC phosphorylation) of the p70S6K-related kinase and its direct activation
CC through T229, also to screen for compounds that inhibit kinase activity
CC in the p70S6K pathway. The protein kinases of the p70S6K signalling
CC pathway are used to define this signalling pathway and to block upstream
CC kinases. Mutation of T389 with an acidic amino acid produces a several-
CC fold increase in basal kinase activity while retaining susceptibility to
CC activation. Use of the new protein kinases in assays means that the
CC signal pathway can be kept active without addition of exogenous mitogens
CC or other activators. The present sequence represents an internal fragment
CC of RAC-PK/Akt alpha containing an S residue at position 6 homologous to
CC T389 in p70S6K
XX

Query	1	PF00571	6	100.0%	Score 35;	DB 2;	Length 10;
Db	2	PF00571	7	100.0%	Pred. No. 1.6;		
Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
RESULT 10							
ADQ74882							
ID	ADQ74882	standard;	peptide;	10 AA.			
XX							
AC	ADQ74882;						
XX							
DT	09-SEP-2004	(first entry)					
XX							
DE	Protein kinase ILK1 assay Akt3 substrate peptide seqid 1.						
XX							
KW	fluorescence-labeled peptide; protein kinase ILK1 assay;						
XX	non-radioactive protein kinase ILK1 assay; substrate; Akt3.						
OS	Unidentified.						
XX							
PN	KR2004009726-A.						
PD	31-JAN-2004.						
XX							
PF	25-JUL-2002; 2002KR-00043762.						
XX							
PR	25-JUL-2002; 2002KR-00043762.						
XX							
PA	(ATMA-) ATMAN BIOSCIENCE INC.						
PA	(HONG/) HONG S K.						
PA	(KANG/) KANG S S.						
XX							
PI	Chun JS, Hong SK, Kang SS;						
XX							
DR	WPI; 2004-458863/43.						
PS							
PT	Claim 2; SEQ ID NO 1; 11pp; Korean.						
XX							
XX							
XX	The invention describes a fluorescence-labeled peptide for a protein						
XX	kinase ILK1 assay and a non-radioactive protein kinase ILK1 assay using						
XX	the same. The assay is useful for easily, rapidly, accurately and stably						
XX	determining the activity of purified or unpurified protein kinase ILK1						
XX	without using a radioactive isotope. A peptide for protein kinase ILK1						
XX	assay is characterized by having the amino acid sequence of SEQ ID NO:						
XX	13, wherein the peptide is selected from the amino acid sequences of SEQ						
XX	ID NO: 1 to SEQ ID NO: 8; and the peptide is labeled with fluorescence. A						
XX	method for determining activity of non-radioactive protein kinase ILK1						
XX	comprises the steps of: labeling a peptide for protein kinase ILK1 assay						
XX	with fluorescence; reacting the fluorescence-labeled peptide with protein						
XX	kinase ILK1; subjecting the reacted fluorescence-labeled peptide to						
XX	electrophoresis to separate phosphorylated and unphosphorylated peptides;						
XX	and determining the quantity of phosphorylated peptide. This the amino						

CC acid sequence of a protein kinase ILK1 assay substrate from Akt3.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 35; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
DB 3 PPOFSY 8
RESULT 11
AAY94724
ID AAY94724 standard; peptide; 11 AA.
XX
AC AAY94724;
XX
DT 29-JAN-2001 (first entry)
XX
DE Antigenic peptide used to raise phospho-specific Ab against PKB.
XX
XX Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1;
KM protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
KM mechanical tissue damage; ischaemic disease; stroke;
KM myocardial infarction; antigenic peptide; protein kinase B.
XX
OS Unidentified.
XX
PN WO200056864-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB001004.
XX
PR 19-MAR-1999; 99GB-00006245.
XX
XX (UYDU-) UNIV DUNDEE.
PA
PI Aleesi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
XX
DR WPI; 2000-647155/62.
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
PT interacting polypeptide.
XX
PS Example; Page 59; 103pp; English.
XX
CC This invention relates to a method for altering the substrate specificity
CC of phosphoinositide-dependent protein kinase 1 (PDK1), by exposing it to
CC an interacting polypeptide. Included in the invention are a preparation
CC comprising PDK1 and an interacting polypeptide, PDK1 with altered
CC specificity is useful for phosphorylating a residue corresponding to the
CC Ser/Thr residue of a substrate with the following peptide Phe/Tyr-Xaa-Xaa
CC Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for phosphorylating
CC protein kinase C related protein kinase 2 (PRK2). The compound identified
CC by methods of the invention that are capable of altering the substrate
CC specificity of PDK1 are useful for manufacturing a medicament for
CC treating a patient who is in need of modulation of the insulin signalling
CC pathway and/or PDK1, PDK2 or PRK2 signalling. A compound that is capable
CC of reducing the activity (i.e. the PDK1 and/or the PDK2 activity) of PDK1
CC may be useful in treating cancer. PDK1, e.g. via protein kinase B and/or
CC SGK, may be capable of providing a survival signal that protects cells
CC from apoptosis induced in a variety of ways. Reduction of the activity of
CC PDK1 may promote apoptosis and may be useful in treating cancer.
CC Conditions in which aiding apoptosis may be benefit may also include
CC resolution of inflammation. A compound capable of increasing the activity
CC of PDK1 may be useful in treating diabetes or obesity, or may be useful
CC in inhibiting apoptosis. Increased activity of PDK1 may lead to increased
CC levels of leptin, which may lead to weight loss. The compounds may
CC suppress apoptosis, which may aid cell survival during or following cell

CC damaging processes and in treating disease in which apoptosis is
CC involved. Examples of the diseases include, mechanical (including heart)
CC tissue injury or ischaemic disease, for example stroke and myocardial
CC infarction, or neural injury. The present sequence represents a peptide
CC used to raise phosph-specific antibodies against protein kinase B
CC phosphorylated at Ser 473. The peptide is used in methods to show that
CC PDK1 is responsible for the phosphorylation of PKB
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 35; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
DB 3 PPOFSY 8
RESULT 12
AAB59262
ID AAB59262 standard; peptide; 11 AA.
XX
AC AAB59262;
XX
DT 27-MAR-2001 (first entry)
XX
DE Phosphorylated peptide substrate #8.
XX
XX Phosphorylation; kinase; insulin.
XX
OS Unidentified.
XX
PN WO200075167-A2.
XX
PD 14-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US016025.
XX
PR 09-JUN-1999; 99US-0138311P.
XX
PR 10-JUN-1999; 99US-0138438P.
XX
PR 08-JUL-1999; 99US-00349733.
XX
PR 28-APR-2000; 2000US-0200594P.
XX
PA (LJLB-) LJL BIOSYSTEMS INC.
XX
XX Sportsman JR, Hoekstra ME, Lee SK, Cairns N, Kauvar LM;
XX
DR WPI; 2001-091201/10.
XX
XX Assay for detecting phosphorylation and dephosphorylation modification of
PT proteins by contacting luminescence peptide with a binding partner and
PT measuring change in luminescence polarization.
XX
PS Claim 13; Page 57; 89pp; English.
XX
CC The present invention relates to detecting addition or removal of a
CC phosphate group to or from a substrate. The method involves contacting a
CC luminescent peptide with a binding partner that binds specifically to a
CC phosphorylated peptide without regard to the particular amino acid
CC sequence of the peptide. The method is useful for detecting
CC phosphorylation and dephosphorylation modifications of proteins,
CC including kinases and phosphatases. The methods can be used to study the
CC kinase activity of different receptors e.g. the insulin receptor and to
CC find agonists and antagonists of these receptors
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 35; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6

```

Db          3 FPOFSY 8
          |||||
RESULT 13
ADR06310
ID  ADR06310 standard; peptide; 11 AA.
XX
AC  ADR06310;
XX
DT  07-OCT-2004 (first entry)
XX
DE  Protein kinase B/ Akt switch control ligand, SEQ ID 8.
XX
KM  Switch control ligand; switch control pocket;
XX  protein activity modulation; human; Akt1; protein kinase B.
OS  Homo sapiens.
XX
FH  Key
FT  Modified-site
FT  /note="This residue becomes phosphorylated upon
FT  activation by upstream kinase regulatory kinases"
XX
PN  WO2004061084-A2.
XX
PD  22-JUL-2004.
XX
PF  26-DEC-2003; 2003WO-US041450.
XX
PR  31-DEC-2002; 2002US-0437304P.
XX  31-DEC-2002; 2002US-0437403P.
XX  31-DEC-2002; 2002US-0437415P.
XX  31-DEC-2002; 2002US-0437487P.
XX  18-APR-2003; 2003US-0463804P.
XX  24-DEC-2003; 53US-00463804.
PA  (DECI-) DECIPHERA PHARM INC.
PI  Flynn DL, Petrillo PA;
XX  WPI; 2004-534376/51.
XX
PT  Identifying molecules that interact with specific naturally occurring
PT  proteins for modulating protein activity, comprises identifying molecules
PT  that bind with the protein at the region of the pocket to regulate
PT  activity of the protein.
XX
PS  Disclosure, SEQ ID NO 8; 204pp; English.
XX
CC  The present invention relates to a method for identifying molecules,
CC  which interact with proteins e.g. enzymes, receptors, or signaling
CC  proteins, in order to regulate the activity of the proteins. The method
CC  comprises: identifying a switch control ligand forming a part of the
CC  protein; identifying a switch control pocket forming a part of the
CC  protein; and which interacts with the switch control ligand, where the
CC  ligand interacting in vivo with the pocket to regulate the conformation
CC  and biological activity of the protein so that the protein will assume a
CC  first conformation and a first biological activity upon the ligand-pocket
CC  interaction, and will assume a second, different conformation and a
CC  biological activity in the absence of the ligand-pocket interaction;
CC  providing respective samples of the protein in the first and second
CC  conformations; and screening at least one of the samples against one or
CC  more candidate molecules by contacting the molecules and one sample, and
CC  identifying small molecules which bind with the protein at the region of
CC  the pocket in order to regulate the activity of the protein. The method
CC  is useful for modulating protein activity and for the identification of
CC  new pharmacological compounds and for treatment modalities. The present
CC  sequence is one such switch control ligand, which is specific to protein
CC  kinase B/ Akt.
XX
SQ  Sequence 11 AA;

```

```

Query Match          100.0%; Score 35; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. NO. 1.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FPOFSY 6
          |||||
Db          3 FPOFSY 8

RESULT 14
AAW34387
ID  AAW34387 standard; peptide; 12 AA.
XX
AC  AAW34387;
XX
DT  04-MAR-1998 (first entry)
XX
DE  PKB C-terminal fragment.
XX
KM  Protein kinase B; PKB; substrate; glycogen metabolism; pancreatic cancer;
XX  regulator; protein synthesis; enzyme modulator; type II diabetes;
XX  insulin-stimulated crosside kinase; breast cancer; ovarian cancer;
XX  therapy; RAC; protooncogene Akt.
OS  Homo sapiens.
XX
PN  WO9722360-A2.
XX
PD  26-JUN-1997.
XX
PF  20-DEC-1996; 96WO-GB003186.
XX
PR  20-DEC-1995; 95GB-00026083.
XX  16-MAY-1996; 96GB-00010272.
XX  18-JUL-1996; 96GB-00015066.
PA  (MEDI-) MEDICAL RES COUNCIL.
PI  (UYDU-) UNIT DUNDEE.
XX
XX  Cohen P, Alessi D, Cross D;
XX  WPI; 1997-341435/31.
XX
PT  Use of protein kinase B for regulation of glycogen metabolism and protein
PT  synthesis - also peptide substrates for PKB and methods for screening for
PT  modulators.
XX
PS  Example 1; Page 11; 98pp; English.
XX
CC  This sequence represents a C-terminal fragment of protein kinase B (PKB).
CC  PKB is also known as the protooncogene Akt, and RAC. This sequence was
CC  used as an epitope to produce PKB specific antibodies. The use of PKB,
CC  its analogues, isoforms, inhibitors, activators and/or functional
CC  equivalents for regulating glycogen metabolism and/or protein synthesis
CC  is the subject of the invention. This sequence can also be used in a
CC  method of the invention for identifying agents that modulate the activity
CC  of PKB. It can also be used to screen for modulators of enzymes that
CC  catalyse PKB phosphorylation. PKB (an insulin-stimulated crosside
CC  kinase) and its analogues etc. are used to treat disease characterised by
CC  abnormal glycogen metabolism and/or protein synthesis, especially type II
CC  diabetes and cancer (specifically of breast, pancreas and ovary). The
CC  various screening methods are used to identify agents potentially useful
CC  for treating these diseases
XX
SQ  Sequence 12 AA;

Query Match          100.0%; Score 35; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. NO. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FPOFSY 6
          |||||
Db          1 FPOFSY 6

```

RESULT 15

AB019480

ID AB019480 standard; peptide; 12 AA.

XX

AC AB019480;

XX

DT 27-AUG-2003 (first entry)

XX

DE C-terminus region of protein kinase Akt.

XX

KM Protein kinase; kinase; enzyme; rational drug design; non-crystallisable;

KM sulindac sulphide; PD98059.

XX

OS Unidentified.

XX

PN US2003032649-A1.

XX

PD 13-FEB-2003.

XX

PF 31-JUL-2001; 2001US-00918873.

XX

PR 31-JUL-2001; 2001US-00918873.

XX

PA (GOLD/) GOLDSMITH E J.

PA (RADH/) RADHA A.

PA (GAYN/) GAYNOR R B.

XX

PI Goldsmith EJ, Radha A, Gaynor RB;

XX

DR WPI; 2003-492076/46.

XX

PT Novel chimeric protein kinase for identifying inhibitor molecules, has
 inhibitor binding site of first protein kinase which bind to inhibitor
 PT and amino acids of second protein kinase which do not bind to inhibitor.

XX

PS Disclosure; Fig 7; 21pp; English.

XX

CC The invention relates to a chimeric protein kinase having an inhibitor
 CC binding site comprising amino acid residues of a first protein kinase
 CC which bind an inhibitor and residues of a second protein kinase which do
 CC not bind the inhibitor. The chimeric protein kinase is useful for
 CC identifying inhibitor molecules capable of affecting the activity of
 CC first protein kinase, by preparing the chimeric protein kinase, growing a
 CC crystal of the chimeric protein kinase, solving the structure of crystal
 CC of chimeric protein kinase, using X-ray crystallography methods and using
 CC the structure to design inhibitor molecules capable of affecting the
 CC activity of the first protein kinase. The structure of the chimeric
 CC protein kinase is useful for the rational drug design of inhibitors of
 CC non-crystallisable protein kinase. The present sequence represents the
 CC amino acid sequence of a protein kinase region near the binding site for
 CC sulindac sulphide and PD98059

XX

SQ Sequence 12 AA;

Query March 100.0%; Score 35; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPOFSY 6
 |||||

Db 7 FPOFSY 12

Search completed: June 14, 2006, 02:09:02
 Job time : 155.5 secs

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:16:55 ; Search time 38 Seconds
(without alignments)
13.821 Million cell updates/sec

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Sequence: 1 fpgfsy 6

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCFUS.COMB.pep.*
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7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	352	2	US-09-771-161A-157
2	35	100.0	417	2	US-09-590-740-4
3	35	100.0	479	2	US-09-771-161A-246
4	35	100.0	479	2	US-09-771-161A-247
5	35	100.0	479	2	US-09-771-161A-248
6	35	100.0	480	2	US-09-091-058-2
7	35	100.0	480	2	US-09-590-740-2
8	35	100.0	480	2	US-09-590-740-6
9	35	100.0	480	2	US-09-538-092-1053
10	35	100.0	480	2	US-09-205-658-157
11	35	100.0	480	2	US-09-526-043-13
12	35	100.0	480	2	US-09-526-043-14
13	35	100.0	480	2	US-09-771-161A-223
14	35	100.0	481	2	US-09-538-092-1054
15	35	100.0	726	2	US-09-417-197-71
16	35	100.0	727	2	US-09-417-197-119
17	32	91.4	401	2	US-09-248-796A-17808
18	30	85.7	112	2	US-09-621-976-5729
19	30	85.7	152	2	US-09-621-976-4568
20	30	85.7	218	2	US-09-270-767-60058
21	30	85.7	449	2	US-10-094-749-2893
22	30	85.7	606	2	US-10-094-749-2892
23	30	85.7	733	2	US-09-328-352-6242
24	30	85.7	788	2	US-09-270-767-44611
25	30	85.7	858	2	US-09-538-092-674
26	29	82.9	59	2	US-09-270-767-40021

27	29	82.9	59	2	US-09-270-767-55237	Sequence 55237, A
28	29	82.9	90	2	US-09-270-767-36421	Sequence 36421, A
29	29	82.9	90	2	US-09-270-767-51638	Sequence 51638, A
30	29	82.9	129	2	US-09-270-767-33659	Sequence 33659, A
31	29	82.9	129	2	US-09-270-767-48876	Sequence 48876, A
32	29	82.9	231	2	US-09-896-522-4	Sequence 4, Appl1
33	29	82.9	320	2	US-09-107-532A-4408	Sequence 4408, Ap
34	29	82.9	320	2	US-09-270-767-42941	Sequence 42941, A
35	29	82.9	395	2	US-09-248-796A-16028	Sequence 16028, A
36	29	82.9	521	2	US-10-155-535-6	Sequence 6, Appl1
37	29	82.9	640	2	US-09-177-165A-30	Sequence 30, Appl1
38	29	82.9	651	2	US-09-248-796A-20333	Sequence 20333, A
39	29	82.9	678	2	US-09-487-558B-314	Sequence 314, App
40	29	82.9	686	2	US-09-134-000C-5066	Sequence 5066, Ap
41	29	82.9	1003	1	US-07-991-867B-6	Sequence 6, Appl1
42	29	82.9	1003	1	US-08-107-755A-6	Sequence 6, Appl1
43	29	82.9	1003	1	US-08-544-332-6	Sequence 6, Appl1
44	29	82.9	1003	2	US-09-370-861A-6	Sequence 6, Appl1
45	29	82.9	1134	2	US-10-154-419-34	Sequence 34, Appl1

ALIGNMENTS

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RESULT 1
US-09-771-161A-157
; Sequence 157, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 157
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-157

Query Match      100.0%  Score 35;  DB 2;  Length 352;
Best Local Similarity 100.0%;  Pred. No. 24;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1  PPGFSY 6
Db      341 PPGFSY 346

RESULT 2
US-09-590-740-4
; Sequence 4, Application US/09590740
; Patent No. 6689607
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 417
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-590-740-4

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 417;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
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Db 406 FPOFSY 411

RESULT 3
US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 479;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||||
Db 468 FPOFSY 473

RESULT 4
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 479;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||||
Db 468 FPOFSY 473

RESULT 5
US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 479;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||||
Db 468 FPOFSY 473

RESULT 6
US-09-091-058-2
; Sequence 2, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; PRIOR FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-091-058-2

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||||
Db 469 FPOFSY 474

RESULT 7
US-09-590-740-2

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; Sequence 2, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-590-740-2

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 469 PPOFSY 474

RESULT 8
US-09-590-740-6
; Sequence 6, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-590-740-6

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 469 PPOFSY 474

RESULT 9
US-09-538-092-1053
; Sequence 1053, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Manfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
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; SEQ ID NO 1053
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P1749
; US-09-538-092-1053

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 469 PPOFSY 474

RESULT 10
US-09-205-658-157
; Sequence 157, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-205-658-157

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 480;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 469 PPOFSY 474

RESULT 11
US-09-526-043-13
; Sequence 13, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 480
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-526-043-13

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 470 FPOFSY 475

RESULT 12
US-09-526-043-14
Sequence 14, Application US/09526043
Patent No. 6881555
GENERAL INFORMATION:
APPLICANT: Guo, Kun
APPLICANT: Pagnoni, Marco
APPLICANT: Clark, Kenneth
APPLICANT: Ivashchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/09/526,043
CURRENT FILING DATE: 2000-03-14
EARLIER APPLICATION NUMBER: 60/125,108
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
US-09-526-043-14

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 13
US-09-771-161A-223
Sequence 223, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 223
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-223

Query Match 100.0%; Score 35; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

RESULT 14
US-09-538-092-1054
Sequence 1054, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratPatSegFormatter Version 0.9
SEQ ID NO 1054
LENGTH: 481
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P31751
US-09-538-092-1054

Query Match 100.0%; Score 35; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 470 FPOFSY 475

RESULT 15
US-09-417-197-71
Sequence 71, Application US/09417197
Patent No. 6518021
GENERAL INFORMATION:
APPLICANT: Ole TRASTRUP, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An Ir
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 71
LENGTH: 726
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PKB-EGFP fusion
US-09-417-197-71

Query Match 100.0%; Score 35; DB 2; Length 726;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
Db 469 FPOFSY 474

Search completed: June 14, 2006, 02:18:40

Wed Jun 14 13:58:13 2006

Job time : 39 secs

09937009-b.ra1

Page 5

Right Page Blank (usps)

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OM protein - protein search, using sw model

Run on: June 14, 2006, 02:33:29 ; Search time 124.5 Seconds
(without alignments)
22.324 Million cell updates/sec

Title: 09937009-B
Perfect score: 35
Sequence: 1 fpqfsy 6 *See 10/10*

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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA Main:
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2: /EMC_Celextra_SIDS3/pcodata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celextra_SIDS3/pcodata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celextra_SIDS3/pcodata/2/pubppaa/US10_PUBCOMB.pep:*
5: /EMC_Celextra_SIDS3/pcodata/2/pubppaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	US-10-014-485A-145	Sequence 145, App
2	35	100.0	6	US-10-148-786A-46	Sequence 46, Appl
3	35	100.0	6	US-10-217-574-6	Sequence 6, Appl
4	35	100.0	6	US-10-217-555-5	Sequence 5, Appl
5	35	100.0	6	US-10-217-555-12	Sequence 12, Appl
6	35	100.0	7	US-09-845-667-12	Sequence 12, Appl
7	35	100.0	10	US-10-317-550-8	Sequence 8, Appl
8	35	100.0	10	US-10-317-550-9	Sequence 9, Appl
9	35	100.0	11	US-10-746-545-8	Sequence 8, Appl
10	35	100.0	12	US-09-845-667-3	Sequence 3, Appl
11	35	100.0	12	US-09-918-873-24	Sequence 24, Appl
12	35	100.0	12	US-10-823-433-7	Sequence 7, Appl
13	35	100.0	13	US-09-845-667-31	Sequence 31, Appl
14	35	100.0	13	US-10-823-433-24	Sequence 24, Appl
15	35	100.0	15	US-09-845-667-29	Sequence 29, Appl
16	35	100.0	15	US-10-823-433-22	Sequence 22, Appl
17	35	100.0	16	US-10-517-904-1	Sequence 1, Appl
18	35	100.0	20	US-10-485-788A-622	Sequence 622, App
19	35	100.0	22	US-10-217-574-22	Sequence 22, Appl
20	35	100.0	22	US-10-217-555-22	Sequence 22, Appl
21	35	100.0	335	US-10-746-545-24	Sequence 24, Appl
22	35	100.0	335	US-10-746-545-37	Sequence 37, Appl
23	35	100.0	336	US-10-217-574-21	Sequence 21, Appl
24	35	100.0	336	US-10-217-555-21	Sequence 21, Appl
25	35	100.0	332	US-09-771-161A-157	Sequence 157, App
26	35	100.0	417	US-10-713-678-4	Sequence 4, Appl
27	35	100.0	479	US-09-771-161A-246	Sequence 246, App

28	35	100.0	479	3	US-09-771-161A-247	Sequence 247, App
29	35	100.0	479	3	US-09-771-161A-248	Sequence 248, App
30	35	100.0	479	4	US-10-394-322A-3	Sequence 3, Appl
31	35	100.0	479	4	US-10-217-574-33	Sequence 33, Appl
32	35	100.0	479	4	US-10-217-555-33	Sequence 33, Appl
33	35	100.0	479	5	US-10-753-267-108	Sequence 108, App
34	35	100.0	480	3	US-09-205-658-157	Sequence 157, App
35	35	100.0	480	3	US-09-771-161A-223	Sequence 223, App
36	35	100.0	480	3	US-09-970-000-4	Sequence 4, Appl
37	35	100.0	480	3	US-09-526-043-13	Sequence 13, Appl
38	35	100.0	480	3	US-09-526-043-14	Sequence 14, Appl
39	35	100.0	480	3	US-09-963-693-157	Sequence 157, App
40	35	100.0	480	4	US-10-060-065-18	Sequence 18, Appl
41	35	100.0	480	4	US-10-059-585-39	Sequence 39, Appl
42	35	100.0	480	4	US-10-394-322A-1	Sequence 1, Appl
43	35	100.0	480	4	US-10-394-568-11	Sequence 11, Appl
44	35	100.0	480	4	US-10-217-574-31	Sequence 31, Appl
45	35	100.0	480	4	US-10-217-555-31	Sequence 31, Appl

ALIGNMENTS

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RESULT 1
US-10-014-485A-145
: Sequence 145, Application US/10014485A
: Publication No. US20020168684A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signaling Technology, Inc.
: APPLICANT: ZHANG, Hui
: APPLICANT: TAN, Yi
: TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES US
: FILE REFERENCE: CST-138 CIP2
: CURRENT APPLICATION NUMBER: US/10/014,485A
: CURRENT FILING DATE: 2002-03-18
: PRIOR APPLICATION NUMBER: US 09/148,712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535,364
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 145
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 145
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MOD RES
: LOCATION: (5)-(5)
: OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated
US-10-014-485A-145

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Cy 1 FPQFSY 6
Db 1 FPQFSY 6

RESULT 2
US-10-148-786A-46
: Sequence 46, Application US/10148786A
: Publication No. US20030143656A1
: GENERAL INFORMATION:
: APPLICANT: Alessi, Dario
: APPLICANT: Biondi, Riccardo
: TITLE OF INVENTION: Protein Kinase Regulation
: FILE REFERENCE: 002.00210
: CURRENT APPLICATION NUMBER: US/10/148,786A
: CURRENT FILING DATE: 2003-01-08
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; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-786A-46

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 1 PPOFSY 6

RESULT 3
US-10-217-574-6
; Sequence 6, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-574-6

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 1 PPOFSY 6

RESULT 4
US-10-217-555-5
; Sequence 5, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-5

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 1 PPOFSY 6

RESULT 5
US-10-217-555-12
; Sequence 12, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-12

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPOFSY 6
Db 1 PPOFSY 6

RESULT 6
US-09-845-667-12
; Sequence 12, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; APPLICANT: Alessi, David
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-845-667-12

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPOFSY 6
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Db 2 FPOFSY 7

RESULT 7
US-10-317-550-8
Sequence 8, Application US/10317550
Publication No. US20030166034A1
GENERAL INFORMATION:
APPLICANT: Thomas, George
APPLICANT: Kozma, Sara
TITLE OF INVENTION: P70-S6K or Related Kinase With
FILE REFERENCE: 4-20793/A/PCT
CURRENT APPLICATION NUMBER: US/10/317,550
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: US/09/297,404B
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-317-550-8

Query Match 100.0%; Score 35; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||
Db 2 FPOFSY 7

RESULT 8
US-10-317-550-9

Sequence 9, Application US/10317550
Publication No. US20030166034A1
GENERAL INFORMATION:
APPLICANT: Thomas, George
APPLICANT: Kozma, Sara
TITLE OF INVENTION: P70-S6K or Related Kinase With
FILE REFERENCE: 4-20793/A/PCT
CURRENT APPLICATION NUMBER: US/10/317,550
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: US/09/297,404B
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-317-550-9

Query Match 100.0%; Score 35; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPOFSY 6
|||
Db 2 FPOFSY 7

RESULT 9
US-10-746-545-8
Sequence 8, Application US/10746545
Publication No. US20040171075A1
GENERAL INFORMATION:
APPLICANT: Deciphra Pharmaceuticals, Inc.
APPLICANT: Flynn, Daniel L
APPLICANT: Pettilo, Peter A
TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
FILE REFERENCE: 34475
CURRENT APPLICATION NUMBER: US/10/746,545
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: US 60/437,487
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-746-545-8

Query Match 100.0%; Score 35; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||
Db 3 FPOFSY 8

RESULT 10
US-09-845-667-3
Sequence 3, Application US/09845667
Patent No. US20020065221A1
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
APPLICANT: Alessi, Dario
APPLICANT: Cross, Darren

TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Braman & Rogalskyj, LLP
STREET: P.O. Box 352

```

; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002,00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-845-667-3
Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
Db 1 PPOFSY 6

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RESULT 11
US-09-918-873-24
; Sequence 24, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radha, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495, 0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; DATABASE ACCESSION NUMBER: P4197
; DATABASE ENTRY DATE: 1996-06-01
US-09-918-873-24

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US-09-918-873-24

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Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
Db 7 PPOFSY 12

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RESULT 12
US-10-823-433-7
; Sequence 7, Application US/10823433
; Publication No. US20050053594A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian Arthur
; APPLICANT: Andjelkovic, Mirjana
; APPLICANT: Cron-Holman, Peter
; APPLICANT: Cohen, Philip
; APPLICANT: Alesai, Darlo
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: RAC-PK AS A THERAPEUTIC AGENT OR IN
; TITLE OF INVENTION: DIAGNOSTICS, SCREENING METHOD FOR AGENTS AND PROCESS FOR
; FILE REFERENCE: 4-20635B/4-20682C/4-33718B/N1
; CURRENT APPLICATION NUMBER: US/10/823,433
; CURRENT FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2002-05-16
; PRIOR FILING DATE: 2002-05-16
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1998-06-11
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 2001-10-03
; PRIOR FILING DATE: 2001-10-03
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 1996-11-05
; PRIOR FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2001-04-30
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (469)...(480)
; OTHER INFORMATION: C-Terminal peptide of Human RAC-PK
US-10-823-433-7

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Query Match 100.0%; Score 35; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
Db 1 PPOFSY 6

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RESULT 13
US-09-845-667-31
; Sequence 31, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:

```

APPLICANT: Cohen, Philip
 Aleesi, Darlen
 Cross, Darren
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
 FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brame & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STATE: New York
COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brame, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
FAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-845-667-31
Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
 |||||
Db 5 PPOFSY 10
RESULT 14
US-10-823-433-24
; Sequence 24, Application US/10823433
; Publication NO. US2005053594A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian Arthur
; APPLICANT: Andjelkovic, Mirjana
; APPLICANT: Ciron-Hofman, Peter
; APPLICANT: Cohen, Philip
; APPLICANT: Aleesi, Darlen
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: RAC-PK AS A THERAPEUTIC AGENT OR IN
; TITLE OF INVENTION: DIAGNOSTICS, SCREENING METHOD FOR AGENTS AND PROCESS FOR
; TITLE OF INVENTION: ACTIVATING RAC-PK

FILE REFERENCE: 4-20635B/4-20682C/4-33718B/N1
CURRENT APPLICATION NUMBER: US/10/823,433
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 10/147,123
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/542,646
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 09/091,109
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: PCT/EP96/04811
PRIOR FILING DATE: 1996-11-05
PRIOR APPLICATION NUMBER: 09/970,000
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 09/068,702
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: PCT/EP96/04810
PRIOR FILING DATE: 1996-11-05
PRIOR APPLICATION NUMBER: 10/673,091
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/845,667
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/091,763
PRIOR FILING DATE: 1998-06-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-823-433-24
Query Match 100.0%; Score 35; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PPOFSY 6
 |||||
Db 5 PPOFSY 10
RESULT 15
US-09-845-667-29
; Sequence 29, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; APPLICANT: Aleesi, Darlen
; APPLICANT: Cross, Darren
TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
 FOR AGENTS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brame & Rogalskyj, LLP
STREET: P.O. Box 352
CITY: Canandaigua
STATE: New York
COUNTRY: USA
ZIP: 14424-0352
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998

APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002,00041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-845-667-29

Query Match 100.0%; Score 35; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPOFSY 6
|||
|||
Db 4 FPOFSY 9

Search completed: June 14, 2006, 02:37:58
Job time : 125.5 secs